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38707 /JJG=H3.288283 Homo sapiens cDNA: FLJ22335 fis, cl udogene, EST3 and ST3 /FEA=CD5 /D8_XREF=gi;2342581 /J	US1 homolog ((5, carevisiae)	AF029669
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38707 /JG=14s, 288283 Homo sapiens cONV. FLJ22355 fis, ch udogene, ESTs and STS /FEA=CDS /DB_XREF=gi2342581 /JJ	P. CHARLES IN CORPORATE MANAGEMENT OF THE CORPORATE MANAGE	MM_W01012
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38707 /J/6=Hs.288283 Homo sapiens cOVA: FU22335 fis, cl udogene, ESTs and STS /FEA=CDS /D8_XREF=gi:2342581 /J	apode deformylase-like protein	NM_022341
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paptiohymotyl isomerase F (cyclophilin F)	BC005020	=
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QAAOS40 protein	AB011112	8.
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vrdescome (prosome, mecropein) activator subunit 3 (PAZ8 gamma; K)	80001423	1.83
COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 7A	AF193844	1.83
epophosis-associated spect-like protein containing a CARD	80004470	1.83
ypothetical protein FU10747	NM_018202	1.83

According to the control of the co	scratch homalog 1, zinc finger protein (Drosophila)	NM_031309	1.83
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Net, 011209 Net, 0	poly (rf.) binding protein 2	NM_005016	3.
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ted factor, 20 kD 105544 20 complete CDS. /FEA=mRNA /PROD=protein-serinethroomina binaze /DB_,RRE=gi-405738 /FL=gb-225430.1 10, NH_, CD3-4065 10, NH_, CD3-4065 10, NH_, CD3-15 10, NH_, CD	capper chaperone for supercide dismutase	NM_005125	<u></u>
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NH_101 9058 U33028	Dnal (Htp40) homolog, subfamily C, member 7	NM_003315	1.81
(U3028 MO07931 NH_Q0163 NH_Q07167 NAQ00635 MAQ0833	MSF-i responsive RTP801	NM_019058	8.
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wantedur protein sorting 16 (year!)	NM_022575	£.
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hypothetical protein FU22.175	AAS51370	67.1
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hypothetical province 112 (00)	B100420/	£ .
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meuroblattoms IAS viral (v-ra) oncogene homolog	NM_002524	£.
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professiona (prosoms, neoropain) 265 subunit, non-ATP ase, 7 (Mov34 homolog)	NM_002811	1.79
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vers grams across or standards states to the state of the state of the state of the standards or state of the	NM_021078	1.79
Mula cyclin-dependent foruse 2 Interacting protein	NM 016550	5 E
cytochroms c addase subunit VIIb pseudogene 1	AF042164	1.78
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rhag finger protein 14	ANU23304 NM 004290	2,7
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APP - thorough inches 13	NM_001659	1.78
SINCE CONTROL OF THE	NM_016333	87.1
done HQQAT7 PROQAT7	NN_018457	2,3
ATPase, N+ transporting, lysosomal (vacuolar proton pump), member J	BC003564	1,78
simulin silent meting type information regulation 2 homolog 7 (5. cerevisiae)	NM_016538	1.78
name onlyine 2, UOA (+) dependent, introductional and the standard of the stan	BC000147	1.78
Common as or repair containing 3 (Surveys)	NM_001168	87.1
deta steep inducing peptide, innrunovaactor	NH 004089	1.78
hypothetical protein DIG-26564K1 42 similar to implantation-associated protein	AL 136636	171
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protein phosphakes 1, regulatory (intibitory subunit 168	6610/456 48020630	3 5
sometoctatin receptor S	NM_001053	1.71
adockto neductase family 7, member AZ (aflatosin aldehyde reductase)	A144075	1.77
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dazapan binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	M15887	<u> </u>
NZEH .	AX026481	1.71
Important Section 3	8000353	1.77
entharyotic translation fatter 25 subunit fatha. 2640)	BC001312 NW 001414	F. F.
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(AR (HR)) RM binding protein 2	PCD03080
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hypothetical protein FU20707	NA_01/936
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chromosome 11 open reading frame 24	AM05185
tubusin-specific chaperone e	NM_U03193
nucleater protein family A, member 2 (NJAKA small nucleater RNPs)	6000003
small nuclear rithonucleoprotein 70kD polypeptide (RNP antigen)	NM_003089
4	80000324
L-call receptor-tosociated protein BAP29	NM_018844
casein binase 1, gamma 3	NM_004384
succinate dehydrogenase complet, subunit C, integral membrane protein, 15kD	AF080579
SWIT ADACT associated regressor protein	NM_015001
General 6400	6003090
cth, garma i	NM_001614
DAMOP43 protein	AL080168
CCTC-binding factor (lanc finoer protein)	NM_006565
condute carrier family 6 (neurotransmitter transporter, GASA), member 13	NM_016615
incompleting the state of the s	BF718610
white from the most domain	KM_003314
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hypothetical protein FL122477	NM_024735	1.57
BQ2/adenovirus E18 1940 Interacting protein 3	NM_004052	1.57
hypothetical protein F1220719	AB051480	1.57
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informer, commandable retain 30	MW AVC223	<u>.</u>
hypothetical protein FU20003	RC00512	<u>.</u>
SWIT protein	NW 006555	
phosphoinositide-3-kinase, regulatory subunit 4, p150	85740111	15.
zine finger protein 216	AF062347	1,51
hypothetical protein MGC10753	NM_016628	1,51
(d3) homolog	AF123539	15.1
polymerze (RNA) II (DNA directed) polypopicide ((3340)	A224143	1.51
VAVY PRESCRIPTION OF STREET, S	AF154847	1.51
Appropriate protein 120396	AF336851	1.51
recursions companies contains a second contains	NN_004623	5
postanem entage gaza cirames, sola-resides autriamity, member 1 postanem entage gaza cirames, sola-resides autriamity, member 1	NM_004979	5.
Speciment symmetries (AMM) 175 (AME - North Specimen Specime Specimen Speci	[423]	<u>.</u>
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karyopherin beta 2b, transportin	BG258639	
gYcogen symbase 1 (masde)	NM_002103	5
DAVIZE FORTIN	AB006624	1.51
Their shock that the	NM_002157	1.51
Control And Contro	BC000354	15.1
Table process	NR_02162/	5 5
ediaryotic transition elemention (action)	MM 004280	<u>.</u>
hypothetical protein MC3180	NN 024041	5
v-erb-b2 arythroblastic leutamia viral oncogene homolog 2, neuro/glioblastona derived oncogene homolog (avian)	X03363	1.51
arthogen-ectivated protein kinese kinese 7	AW007458	15.1
XI domain and marinet transposate fusion gene	NM_006515	1.51
Impromeduate provine for Library to membrane protein, palmitoylated 3 (MACIN p55 subtamity member 5)	NH_022474	1.51
Appropriate for the second sec	NM_018346	1.S.
provides when you make a condemnativities even a first of and 0.0 per provides and the provides a condemnativities even a first of the	MA_003541	2 5
behalfor which describes and many to the compensation groups A. L. and U.). The compensation of the compe	082828	9.5
COMMUNICATION OF THE PROPERTY	A8023216	8.5
	21 77000	<u>}</u>

	OX (6 cell division cycle 16 hampleg (5, cerevisiae)	AF164598	2. S.
	DELOM (vep-ba-As-AspAris) box polypeptide 16	N36997	<u>.</u>
	rigidate-encicles factor 1, april a source (see feature) and the conference of the c	NM_001530	8.5
	provincement (provincement memoryben) cas submitte (provincement provincement provi	MA_00280/	R 5
	Institute of the state of the s	MA 046346	R 5
	(AA0339 order)	MM_015113	Ŗ <u>5</u>
	Percentification contains to be a breached a family	SOURCE MA	3 5
	City describes	RCM1286	R 5
	entain	8001906	3 5
	enhibitor of DNA binding 2. dominant necessive heliz-loco-heliz protein	MM 002166	3 5
	Propobetical protein MGZ745	NM 024117	3 5
	Conseque includes chall 1990 AFFamer ON 1865 and 14300 MR 1865 and 111 MR 1865	131807 6 AW128903	3 5
	where the state of	2000 HM H 1000 20	2 :
	Committee Commit	MH_003656	3 5
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	TOTAL STATE OF THE	A5023215	<u>S</u>
	NO ENACE	A334128	<u>S</u>
	cathern, Elf LMs seven-pass 6-type receptor 1 (flamings homolog, Drosophila)	BC000059	3.
	viral matter surcome 36 il viral oncogene homolog i	NM_001654	3 .
	KAN binding protein 2	D42063	3.5
	tyrasine 3-manoarygenase/frygkaphan 5-manoarygenase activation protein, beta potypeptide	BC001359	35
	coolad vesicle membrane protein	NM_006815	3 .
	alanine-gyonytide aminotransferese (ozalosis I; hyperozaluria i; glycolicaciduria; serine-pyruvate aminotransferase)	013368	S. 1
	NABGB, member RAS oncogene family	BC002510	8.
	hypothetical protein MG(10940	BC004331	35.
	Down syndrome critical region gene 2	NM_003720	<u>3.</u>
	hypothetial priviles	NM_015705	5.50
	Section 5 protein	AK026025	3.
	MAZ protein	NM_025259	<u>.</u>
	mtogen-ectivated protein lahese lahase lahase 7	NM_003188	<u>s</u>
	ets verlant gene 5 (ets-mated molecule)	BF060791	3.
	Consentus includes gb:AZZ-4869 (DEF =Homo sapiens CKR4 gene encoding roceptor CKR4 /FEA=mRNA /DB_XREF=gi:3059119 /UG=Hs:89414 chemokine (C-X-C motif), receptor 4 (husin	4 (fusin Al224869	3.
	denombed for herelog 1 (MP1 beta homelog Dresophila)	NM_006807	3.5
	nucleoporn KZd	NM_012346	.5s
	programmed cell (each). 2	NM_002598	. .
	Prpoducial protein FU12171	NM_024619	<u></u>
	U.Z. artigen	759350	.
	2 perus gradunos	AL513611	3 .
	kayopherin (imporin) beta i	86545463	8.
	histofine trad nucleobide brading protein	N32864	1.50
	and contribution (A) in leucines	AV712577	05.1
	LIAND'S gene product	NM_014824	3 .
	E.D. vasicipon later	M96577	2 .
	UNIVERSE PROBEIN	AA868332	<u>S</u>
	Authority Christian Inches 44, Bottom 2	796100 MM	S; ;
	scenario de la companya de la compan	NM_024815	8:
	programmy required to the standard but the standard of the sta	AP0//198	8 5
	Proceding the programmy content of the process of t	NA 02480C	<u> </u>
	importus (influenza) resistance i, bomolos of murine (interferon-inducible protein p.78)	NH 002462	3 5
	(ZAL1194 protein	NA 015455	9
	distant-Consyme A dehretocense	NM 013976	4
	hypothetical protein FLU13660 similar to CDKS activator-binding protein (53	NM 025197	9
	KDA60056 protein	A796581	69.1
	16.71/d protein	NM 016139	67
	panoratic polypopide	M15788	1.49
	gb/#308302.1 /DEF=Homo supiens serologically defined breast cancer antigen NY-BR-96 mRNA, complete cds. /FEA=mRNA /PROD=serologically defined breast cancer antigenNY-	8R-96 / AF308302	1.49
	Consensus includes gb.M.134724 FEA=EST /OB_XREF=gi:6602911 /OB_XREF=ext:DKT25547P246_51 /CLONE=DKT25457P246 /UG=Hs, 4988 Homo sepiens clone 24711 mRNA sequence A.134724	equence AL134724	1.49
	Nacent-polypeptide-essociated complex alpha polypeptide	NM_005594	1.49
	IAU2O homolog (3: cerentale)	KM_005732	1.49
_;	District Control (Tarm Induction (MADPI))	NM_000713	67:
7	Jambar 1974 of protein freedy belief freedy micro freedy	NH_UUSS63	6
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dromodes herrolog 3 (IPT gamma hornolog, Drosophia)	BE748755	64
nuclear receptor co-repressor 2	NM 006312	69.
gadgin-67	AF163441	69.1
Commensus includes gb:8E671941 #Eb=E57 (08_XREF=gi:10032405 /08_XREF=est:7a46602.a1 /RIOME=INAGE:3221810 /MG=Hb:157078 Homo sapiens (DNA FU17293 fis, done NTZRI 66671941	28! BE671941	\$
algoral recognition particle 7260	AF069765	64.1
OCC16 call division cycle 16 homolog (5. cerevisiae)	AF164598	1.49
ribonomal probain S6 kinses, 9000, polypopide 1	NM_002953	49
phosphorytae finance, gamma 2 (testis)	NM_000294	1.49
Institute II Contain profession 2 stratelli, bounded of Informacebilin	KM_002518	. .
RO 2/zdenower Et 1990 interaction contain	MM 043078	
professional (prosona, enchosais) 265 subunit. Al? see. 2	MM 002803	
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zinc finger protein, substantly 1.A. 1 (fluence)	•	£.
disphaneus homolog 1 (Drosophila)	60	1.49
ADP -theosytemese (NAD+; poly (ADP-those) polymense)-like 2		1.49
CONTRACTOR MONOGO SON METERS 1 (08 JACE = 9:143/01 / /08 JACE = estate-4cc0s.s1 /(LONE=HARE: 362030 /(Je=Hs.59839 E37s, Weakly similar to (GHU/1 collagen alpha 1 (III A000152)		Q :
any output managed as a contract of English	AW05018/	\$
Consensus includes on PA 1999; 10EE Human 181 once mBNA 3 and, FEA mBNA AEN = 181 AB 10B 188E = 112400 AE = 14 75539 Human 181 once mBNA 3 and		9
sorting near 17	\$	9
RAMOGS gave product		1.49
KAM2258 gene product	NM_014785 1	6+.
armodevinited (all pyth) as a factor of the control		3
Appendix protein FLI10509	6	3
urendes research guinne franctione-certaing process. c	AV65/604	9 5
ribosomal protein S4. X-finland		3
cyclin-dependent kinase (IDC2-litte) 10	AF153430	₹.
Conservate includes gb: 166 170559 FEb=EST /08 JOEF=91:12677362 //08 JOEF=est-602323331F1 / ALONE=IMAGE:4426926 //UG=Hs.226138 Homo supiers mRNA; cDNA DIPTp566H244	BG170659	2 .
Vydorovne codose subani VII a polypepide z kka Inmeritacije i receja, El 1714s		9 9
nwideer transcription factor, 2-box binding 1	NN 002504	ş ş
ribonomal protein U	_	.
seruticipically defined colon cancer artispen 8		₹.
integral, apple 4 (antigen CM90), alpha 4 subunit of VLA-4 receptor)		3
by the promise process to the process of the proces	RF244411	7 5
caysterd bloding protein		3
endumyodic translations initiation factor 3, subunit 10 (theta., 150/170kD)		2
nuch (nucleoside diphosphate linked mointy XI-type motif 9		5 .
drawboar homolog, (Presphila)	·c	\$!
production to receive the second seco	BC00253 1.	2 9
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FUS interacting protein (serins-arginine rich) 1	-	#
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THE STANFACT STANFACT	U30\$72	84.1
entropine forms (ALRO) homology and (ALRO) hom	AW241715	2 .
Newsytaphingsiase amiddity-drottese (acid coramidase)-lilie	AK024677	2 :
reposits, light polypaptide, regulatory, non-sercomeric (2040)	KM_006471	3 :
ATPase, Ne+/K+ transporting, alpha I polypeptide	NA_000/01	<u> </u>
ON 27 Section 2	AI986295	3
NUMBER OF PERSON AND A COLUMN A	NM_003646	\$
Investigation of the control of the	AL136619	 84.
artigan Identified by monoclonal antibody Ki-67	AU147044	2 :
hypothetical protein FU13441	KM_023924	3 :
tropora chunnel 1, homidog	KM_01/901	3 :
Consensus includes gb.X69637.1 (DEF=H1 supiens mRNA sequence (16p11.2). (FEA=mRNA /OB_XREF=9:29573 /UB=H3.30/208 H3speens minha sequence (19p11.2)	A0703/	? 5
URA domain-containing 1	NM_015845	2 5
mentary can be burding domain protein I	042043	3
workerson processing the second secon	M566096	 8
hardings on coming process	NM_023071	34.
Inference syndrome critical region cene DGSI, libely ortholog of mouse expressed sequence 2 embryonic lethal	NM_022719	3.
waste triffiction, bach and arriver containing	W60686	3.
halocytochrome c smithase (cytochrome c heme-lyase)	NM_005333	2
hypothetical protein FU10540	NM_018131	-
oruldane decendor/tae entisyne inhibitor	A047234	3
eutharyotic translation factor 3, subunit 7 (zeta, 66/67AD)	MM_003753	9 9
heat shock 60kD protein 1 (chaperonin)	NM_002003	2 9
OX-Mis interes 2	AA478965	
THE EXPLANATION OF THE PROPERTY OF THE PROPERT	NM 018129	•
Approximate protein 1 U1033	AF155159	4
MAINTENEMENT PRODUCTION OF THE CONTRACT OF THE	AA886971	1.47
destri	NM_001927	1.47
prp.28, US anRNP 100 kd protein	NM_004518	4
tuffalin-interacting protein	A220627	<u> </u>
Float only protain 3	MM_0121/3	2 5
Communic apt. ALCH 2007 DEF = Home supiers mRNA; CDNA DIV. 2564F112 (from clone DNV 42544F112). /FLX=mRNA /DB_AXEF=GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. Too.Set From Supers mr x, Layson (communic includes apt. ALCH = GF-4684C36 /Us=HS. T	N 017999	9
Typichesia protein 101011	969900 MN	2
Physical conditions are applied to the control of the condition of the con	NM_016125	1.4
Conserva includes the ID11995 OFF = Human DIA sequence from clone RP1-269415 on chromosome 20s12-13.12 Contains a gene similar to peptidyforolyt isomerase (cyclophilin), part	_	1.47
34 (bechnia centachts synthese) ilte		1.47
Consessus includes gis.143577 FEA=EST (AB_XREF=g:899066 /AB_XREF=est:143577 //LONE=EST500 /UG=Hs.82171 Home sapiens (clone 115392) mRNA	143577	- :
cell division cycle 250	NM_001790	2 9
IAPI, GTP-60P desociation stimulation	AL 137750	9
COUNTY LINES	NM_014267	1.47
CEA-ACT transcription complex, subunit 3	AF180474	1.47
broanddomain adjacent to zinc finger domain, 18	A1826454	G !
basis transcription factor 3	X/40/0	<u> </u>
memic fiftings formation (functional and functional	NM 005926	0
Reported process Personal Common Personal Co	NM_006227	1.47
Proportional Control of the Control	NM_024946	1.47
parinergic incisptor P21, 6-protein coupled, 11	NM_002566	(+1)
microphage inyritorylated slamine-rich C thrase substrate	KM_023009	÷ :
Acry repair complementing defective repair in Chinese hamster cells 3	NM 015710	3
gloom turns supported randoms region gene 2	KM_024073	3
influenced promise receipt in a second of the second of th	BC002411	1.47
Fredbyth state	NN_000144	1.47
apolipoprotein M	AF161454	G !
Consumes includes go. WOT 18 (1 / DEF = Home supiens CDN, FU 10954 fs, clone PLACE (200383, highly similar to Home supiens mRNA for MTMR I protein. / FEA=mRNA / DB_AREF=gr.70 a MODI 816	C AKOO1816	<u> </u>
profesh photophase 2, regulatory subunit 8 (856), epsilon isoform	78260	. 4
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I'M receptor-essecuted factor?	O I	W_021138	(
membrane associated tyresines and threemine specific cot2 inhibitory timase	O I	NM_004203	.
Companious includes gb./A907003 /F.EA=EST //UB_XKEF =g:6497611 //UB_XKEF =estrPM:B1134-050499-650 //UB=HS.124620 ESTs	A90/083	.083	- !
Zint finger protein 131 (done pHZ-10)	AW967	AW968301	1.47
threedectide repeat containing 5	80004423	#53	1.47
symplektin; Nurtingtin Interacting prot ein 1	0,12	NM_004819	42
interleutin enhancer binding factor 1	SEN	NM_004514	1.47
(GL 99 protein	O EN	VM 016039	1.43
Preschedule protein FU13220	S EN	NM 021927	1.43
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observations (idea - reculatory suburit coherentide (05 alpha)	A580192	1192	140
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of historical features of the state of the s		2000	2 :
UEAU/H (ksp-elu-Ke-Ksp/kis) box polypopidoe 11 (tht.1-tike hekcase homolog, b. cerevisiae)	D_MM	NH_030653	\$
hypothetical protein DRP 20564004 78	AL 136633	5993	9
nuclear transcription factor T, alpha	AL031778	2//2	9
onfolion resistance 1	IO_MX	NM_018002	-
heat shock 90kD protein 1, alpha	AF028832	1832	4 .
matallothicnein 1H	AF333388	3388	9 .
CDC14 cell division cycle 14 homolog A (S. cerevisiae)	AF064103	1103	1 .46
pleaminogen	M74220	20	- ,4 6
heme-regulated initiation factor 2-siphs lithuse	IO WW	NM_014413	.
Propoliteixal protein. clone Telethon (Bah. 841). Strait02270 Ft142	NW 02	NM_020247	1.4 6
odaneous T-cell Imminoma-essociated fumor entition se20-4; differentially expressed nucleolar TGF-beta I target protein (DENTT)	NN OS	22117	9.
adentitie A2n receptor	8 8	NM 000675	94.
code secretable common selection on containing ARF binding nearlier 3	AWOOSOIS	8018	4
DETP 115 (08 market)	RE222901	1060	44
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Unal (1sp44) homolog, subtamily 8, member 6	A-080569	6	2 :
Official	IO NA	KM_018116	\$
entochondrial ribosomal protein L49		04927	.
Ouster Incl. MS24093ng33104.s1 Homo septions cDN4.3 and /clone=IMAGE-936607 /clone_end=3 /gb=MS24093/gi=2265021 /ug=Hs.23158 /nen=718		1093	.
hypothetical protein FU22246	NM_02	NM_025232	.
profykarboxypeptidase (angiotensinase ()	DO_MM	05040	1.46
WW domain binding protein 2	U79458	5 2	- ,
hypothetical protein FLI 10659	KM_018171	18171	 5
hypothetical protein FL/13949	NM_025077	25077	.4 6
MAA0429 gene product	AF116674	674	-,46
spectric apha, non-erphrocytic 1 (alpha-fodrin)	AL110273	273	-
hypothetical protein MGC4172	NM_024308	24308	4 .
Appropriate Approp	90, MN	04925	2
Consensus Includes gb: W95043 /FEA=EST / OB_XREF =g:1424182 / OB_XREF =est:zh46c1131 / CLONE=IMA6E-415124 / U6=Hs. 79732 fbulin 1	E#050#	e :	\$
Tark Brigar process 2.28	77.77.W	7	? :
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MINISTER ESCOCIATION OF THE PROPERTY OF THE PR	OCCIOCAL IN CA CHICAGO	8 8	€ :
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hypothetical protein FLI 4972	WESTON	66.	? :
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### (2017) ### (2	Social F	STAM MU	
Science protein 1) 1. subunit & (344D), done MGC:11274, mRNA, complete cds. /FEA=mRNA /PROD=Similur b. 1 CLONE=IMAGE:1172248, /MG=Hs. 170218 KUAN0251 protein A A CLONE=IMAGE:1927473 /MG=Hs. 469 succinate dehydrogenase complex, subunit A, flavopa A M N N N N N N N N N N N N N N N N N N	ant transforming growth factor beta binding protein 4	EZSEON MA	
ACTORION (1973) ACTORION (1973) ACTORION (1973) ACTORION (1974) ACTORION (1974	stathione transferase zeto 1 (malerlacetoacetate isomerase)	6760074	
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### (2002) ### (2	1	Z6086ZHY	
## (1940), done MGC:11274, mRNA, complete cds, /FEA=mRNA /PROD=Similar & B(0002878) ## (2017) ## (2012) ##	The state of the s	AF276920	
##_Q02773	The state of the s	BF341845	
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rdin sensitivity conferting protein) 1341.092 (from clone DKS2p434L092). /FEA=mRNA /OB_XREF=gi:6807951 /NG=H1.306457 Homo sapiens mf olase)	hypothetical protein	AF217514	2
1341.092 (from clone DKF.Zp434L092). /FEA=mRNA /DB_XREF=g;6807951 /UG=H1;306457 Homo sapiens mf	ATP synthase, H+ transporting, mitochondrial F1 complex, 0 subunit (oligomycin sensitivity conferring protein)	577356	1 37
1341.022 (from clane DK52p4341.092). /FEL=mRNA /OB_XREF=gi:6807951 /UG=H1.306457 Hamo septiens mf olizee}	galgi SWV receptor complex member 2	BE895285	1.13
1341.092 (from clone DK72p434L092). /FEA=mRNA /DB_XREF=gi:6807951 /UG=Ht.306457 Homo sapiens ml olase)	6 protein-cupled receptor 87	NM 023915	1.37
1341.092 (from clone DKZ.p4341.092). /FEA=mRNA /D8_XREF=gi:6807951 /JG=H1.306457 Homo sapiens mf olese)	pitultary tumor-transforming 3	KM 021000	1.37
1341.022 (Irom clone DKZ. p 4341.032). /FEA=mRNA /DB_XREF=gi:6807951 /JJG=H1.306457 Homo sąpiens ml ołace)	guarine nucleocide binding protein 10	NM 004125	1.37
134(092 (from clane DNF2p434(092). /FEA=mRNA /OB_XREF=gi:6807951 /UG=H1.306457 Homo supiens mf olase)	KDA0295 protein		133
disce)	Consenses includes gb:AL137403-1 /0EF=Home septions mRNA; c0NA DNF2A434(092 (from clone DNF2A44,092), /FEA=mRNA /0B XBEF=ai:6807951 /UE=H1.306457 Home sanie		13
	acetyl-Consyme A acytransterase 2 (mitochondrial 3-ozoacyl-Coenzyme A thiolese)	111900 NN	2
	Protein P3	NM_019848	1.37
	small nuclear ribonucleoprotein polypeptide (NM_003093	1.37
	zinc finger protein 36, (3H type-Like 1	86250310	1.37
	mannesy (aphe 1,6.) gyroprotein bels-1,2.N-schydykosaminytransferase	8(006390	1.37
	/ under	NM_014296	1.37
	e. Z to protest	NM_019059	1.37
	Tar upotraum generat (FUX) briding protein 3	069127	1.37
PRINCIPATIONS BINCHER 8 NN_002854	retrictivate briding protein 8	NH_002894	1.37

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	PERMANENT OF THE CASE AND ASSESSMENT OF THE CASE ASSESSMENT OF THE C		2 :
	CONTRIBUTE AND POST OF THE PROPERTY OF THE PRO	NA_004399	1.37
	Commens included () UCF = Human DNA Sequence from PAL 130k2 on Chromosome 6p.Cz. ZZz. 3. Contains ribosomal protein L29 pseudogene, ES13 and S135 /FEA=mRNA /		1.37
	United from the face paid in the face of t	KM_016213	1.37
	Thoseonal protein XT	AW024383	1.37
	95/13610.1 / UEF = Human PACAP type-31/P type-31/P type-2 receptor milkA, complete cds. / FEA=mRNA / PRO0=PACAP type-31/P type-31/P type-2 receptor / 08_XREF=g;:1684934 / FL=gb:U18810.1	018810	1.37
	MTC-essociated zinc finger protein (purine-binding transcription factor)	NM_002383	1.37
	hypothetical protein FU11240	NM_018368	1.37
	potassium channel, subfamily K, member 13	NM_022054	1.37
	separt/ducosaminidas	NN 000027	1 33
	IGMO732 game product	AWS:0783	2
	c-max binding protein	41 526413	1
	safety assembly for the same managed of the same managed of the first the same managed of the same and the same of	ASSAIL	6
	The state of the s	NM_003131	1.37
	C USAN DE CONTROL DE C	W675900	1.37
	hypothetical protein FL10849	NH_018243	1.37
	KQA1052 protein	956710 MN	1.37
:	apioid growth factor receptor	NH 007346	1.37
	Procupitizal cretain [1173394	SESSES AN	
	The second secon	NM_030825	6
	and yet restoral manual association, which is a community of member 4	A8316/5	1.37
	protein prospitation (, ingulation) (inhibitor) subunit 13A	NM_014330	1.37
	ATPase, Ca++ transporting, type 2C, member 1	AF189723	1.37
	Consensus includes gb: M275383 /0EF = Homo septens partial (6VH3) gene for immunoglobulin heavy chain V region, case 1, cell Mo IV 72, /F.EA=(05 /0B_XREF = qi:7573027 /ule=Hs.272383 M275383	35! Al275383	1.37
	hypothetical protein FU20160	NM 017694	1.37
	translocation protein 1	1193239	
	considerations is neuronal 2. Late in Janeire Blancko Richeckowsky diseases	44603633	
	Annual state of Annual Annual State of Annual	W006336	<u> </u>
	Section Control of the Control of th	W023260	.36
	L METADOREI	NN_017927	1.36
	Suppressor of Ity & homolog (3, cerensule)	A494567	1.36
	702-binding thisse, 1-4el ongoinated protein tinase	NM_018492	1.36
	KAAO406 game product	AB007866	1.36
	stand O-exptransferase (expt-Coenzyme A: cholesteral exptransferase) 1	121934	1.36
	actio creas-limbing factor	A8029290	1.36
	ribbaomai protein L41	NM 021104	1.76
	dhromosome 11 hypothetical protein ORF4	AA479495	2 2
	mule-enhanned antigen	NA 014623	¥.
	Fine (TMFRSF) exacociated factor 1	NM 007051	2
	PDA0365 gave product	RCSCSES	2 2
	CMS brighet repost, RIVA binding protein 1	NH DOGGO	2 %
	ubiquitin-conjugating enzyme E2 variant 1	4) 121673	3 %
	Of the total of the description (actor)	A.1210/3	<u> </u>
	brothetic green 243	03685	9 3
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	hand shorts for cortain 20 (mortain 2)	A 231062	e :
;	uncharacterized bone marrie protein BH046	NH O18450	36.
	sulkrine factors 3b, submerit 1, 1550.	AM DESCRIPTION	97.
	contine administratories macle	NA_012433	ę ;
	ribosomi orden (2)	UN 003064	9.
	membrane colator protein (CO46, trophoblast-tymphocyte cross-reactive antioen)	41570661	2 7
	ubication-contrasts entree E26.1 (UBC) homeloo. C. elecans	1000125	P
	Propomodulia 3 (ubiquituus)	WM OSSEST	9. 1
	Interrogeneous nuclear (Bonucleoprotein H3 (2H9)	AE(22)362	2
	caribasomal protein 2	AF022655	2 2
	hypotherical protein FL10307	NN OTFOS	¥ .
	CGI-02 protein	NW 012123	2 2
	3-hydray-3-mathydydayl-Conizyme A roductase	NW ODG859	2 2
	nuclear phosphoprotein similar to S. cerevisiae PWP1	NM 007062	2 %
	exportin (CRN I homolog, years)	089729	95.
	hypothetical protein FLL21945	NH 025203	36
	IQM0193 gene product	NN 014766	92
	IQMO483 protein	NN 015176	1.36
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Alland Comments	AI 5,814.73	1.36
MXVI to profession 1 MX 6 according to 10 MX 1 M	N472757	1.36
emorphic factor 1, heading LF-81, heading nuclear factor (NMF1), albumin proximal factor	M57732	1.36
Immunite 3-monocrypanase (Immunite 3-mydrox/lase)	A074145	1.36
Proodhelical protein F.110466	NN_018100	1.36
(DAGC) Erretain	KM_015043	1.36
phosphomenoruluse 2	KM_000303	1.36
Manein A, alpha (actin binding protein 280)	NW_001456	1.36
rat froger protein	AL523814	92.
protein phosphalase 1, regulatory (inhibitor) subunit 2	24.996.49	4 3
Comentus includes gb.28 0246 Wathers clabitin light chain a gene, ITEAS mRINA (08, XAEP = 9; 704460 (VG=15, 25568 H. Sapiens clatinin light chain a gene	969197	2
COTS (constitutive proteomythogenics, Arabidopsis, homolog) subunit 4	NM_016169	95.1
malancem angels, lamily A, 12	NW 001283	98.1
anaptor-related protein complete 1 sugment Subunit	603100 MM	2 -
UNION (Appellation Particular) and polyperione 10 (Min see a constitution of the const	1182278	
HARBOCYTE INTUINOSCIONAL SUBSTAINT, NAT. I N. COMUNI), MEMBER 2	NM 020998	<u> </u>
a manufacture annuacing 1 (maparacyte grown textor-line)	NM 018447	1.35
An about proceeding the control of t	KM 014937	1.35
AMERICAN STATE OF THE STATE OF	NINE N AA650558	1.35
Andrea III	NM 003909	1.35
suppose Prosecription barbon 2 sites interaction	130824	1.35
Updates a catalogical taxon at the same and a same actual at the same at the s	AX025122	1.35
A however the property of the	AF176699	1.35
hemsine 3-enconveness bruttanhan 5-monoanvenase activation protein, excilon polyneotide	U43430	1.35
formal critical 11	NM_000993	1.35
Comments includes ob AA721005 (FEA=EST //B XXEF = c1:2737160 //B XXEF = c1:n189405.s.) ALONE=IMAE-1269464 //JG=Hs.293253 ESTs	A721025	1.35
transferze of inner mitochondria membrane 44 homoloo (vess)	AF026030	1.35
v-ch sarcons viris (T10 oncoore homoloo (aviar)	NN_016823	1.35
defension beta 2	NM_004942	1.35
translociate of inner mitochondrial membrane 22 homolog (yeast)	NM_013337	1.35
IQA0240 protein	AJ801951	1,35
putable 6-protein coupled meaptor	MM_016334	1.35
KF-II mtN-binding protein 3	AL023775	S :
SELENDMOSPIATE STRITHETASE ; Human selenium donor protein	AV6826/9	9 1
protein kinese C, derta	KM_006254	9
uncharacterized hypothelems protein MMP I i	ANU22246	5
Layopherin (importin) beta 3	A4214406	5 5
Dyracid Antonion Resignation Lessociated protein, 35-kD subunit	BC002449	
American prices (Library 1981)	NH 003746	135
All assessment, the programmer and the second secon	A799802	1.35
small nuclear RNA activation complex, polypeptide 3, 50(i)	071300	1.35
Wall-Hinchhom smartum candidate 2	NH_00563	1.35
HGC6.1.1 protein	AB016900	1.35
IGAA0355 gene product	NH_014686	1.35
With transcription factor	114077	<u> </u>
Arms Andrew (The Control of the Con	1036344	
The state of the s	AW268585	1.35
hearth is a principle of the second of the s	AF151022	1.35
owners transmission latter II.	AC004883	1.35
unduranterized hemetopoleids stem/progenitor cells protein MOSO28	NH_018463	1.35
spiking factor 1	NM_004630	1.35
GATA binding protein 3		1.35
Consensus includes gb.AW373379 /FLA=EST /08_XREF=g1:72.46918 /08_XREF=estill.HF-810.ack.et-05-0-UI.s1 /KLONE=IHARE:3060969 /UG=HS-ESS1 ATP-asc, H+ transporting, hysoson		£ .
enghtes-promoting complex subunit 10	COOK OF ANY	5
hypobacias projem ILLS 177 **Marks projem ILL	NMU22U63	
COMMING MICHAEL GOAR 1 CASH 1 (NO ARE SELECTION OF THE SE	NM 014181	1.35
That is a second entered and e	NM_016839	1.35
Franchistical costs and 13729	278330	1.35
potassium channel modeldowy factor	NM_020122	1.35

Pypothetical pratein	NM_018988	1.35
Grading opposite 33	NM_001507	1.35
Indicators related to the control of	NM_018169	S 5
interacto 2	AF182198	
tetratricoperdide repeat domain 3	083077	1.35
nucleer pore complex interacting protein	AF229069	1.35
Library neutrals facts, although and protein 2	A862445	1.35
ECUAL (2) - Decorate protects (34 excessory protects (2) ECUAL (2) - Decorate protects (3) ECUAL (AW575374	5.3
dynamicans 5 cars making three 6	NM_01660E	35.
UDP-H-cter/ducosamine prophosophoritae i	573498	56.
ATP divine lyine	A971281	1.35
nuclear cup binding protein subunit 2, 20kD	80001255	1.35
hypothetical protein FU23459	HM_024775	1.35
FUS interacting protein (servine-arginine rich) 2	KM_021993	1.35
International Leaf Annual Control Co	NM_006519	55.
An Unitarian socialism (AU)	A8011178	£ :
1954 modesty	RC02976	5 2
IQM0648 protein	AW991219	7
MTB binding protein (P160) 1a	NM_014520	5
zinc finger RNA binding protein	BC000376	¥.
add-intension (5.43-containing protein)	AF260261	7
ELAMOS CAL POTENT F L10/V3	NM_018188	¥.
vacular modernial growth factor	M27281	* 7
hypothetical protein F122222	W1968	7
cation channel, voltage-dependent, gunna subunit 2	AL022313	3
transcriptional intermediary factor 1	AL538264	<u>*</u>
CLANOR 10 protein	BE615699	7.
CONSTRUCTION OF THE STATE OF TH	AA928506	X
general Vertificat « debonomal reveitin I s	AF080586	<u>*</u>
Consensus includes do:85466235 FEA=EST 400, 1385-1951025 AEA-EST 400 15320 AEA-EST 400 15320 AEA-EST 400 AEA-EST 4	ANUC/146 03: BF466525	<u> </u>
splicing factor, arginine/barine-rich 4	NH_005626	134
emi i sequence (mammany tumor and squamous cell carrinoma-associated (p80/85 src substrate)		¥.1
CONSISTED INCLOSES 90:307/42/OEE = Human autonomous replicating sequence H1 (ARSH1) /FEA=(D5,/DB_XREF=9:179028 /UC=15,247945 Human autonomous replicating sequence H1		1.34
recommendence 1 cycles American Section Ameri	KM_022338	<u>.</u>
production while process in the contract of th	U16953	3 3
	AKD21546	5 2
etoposide-induced m@NA	NH_004879	1 7
Consumus includes gb:18669922 FEA=EST NB_XREF=gi:10318698 /NB_XREF=est:601446568F1 /CLONE=INAGE:3850432 /NG=H3.181307 H3 histone, lamiy 3A	BE869922	1.34
NAVO (Percent	AK026096	<u>*</u>
perunisonal 0.1.02 -enoy-(-to/ isomerae	A300084	* * *
Consensus includes goldL049250.1 (DEF=Homo supiens mRNX, cDNX DKEQ564D113 (from clone DKTQ564D113). FEL=mRNX, //B_2/REF=q;-4499989 /UG=Hs, 194637 BANP homolog.	٠,	<u>.</u>
Sec23-interacting protein p125		134
symmetric and statement i constructions at properties () (glaucoma 3, primary intantite) Interior national administration and the administration of the statement of the statem	N21019	1.34
circus (service difference a) general difference indee 21	BC001120	4 2
rabs of Pasa extrating protein (6AP and centrosome associated)	NM 012197	<u> </u>
LOV The prophosphoripes	AL 1 10209	ž
WR (a-hakis colled-cell red homologue)	AB029343	¥.
Verify (Manages) missing on the control of the cont	NM_002467	¥.
MAINTENANCE PORTION OF THE PROPERTY OF THE PRO	A ANT-4059/4 AF205218	<u> </u>
ribosomal protein 137a	NN 00098	<u> </u>
KGA1097 protein	A8029020	Ž
IRM binding motif protein 15	NM_022768	1.34
hypotherial protein H(33)7	AX021779	£.
VIO.5 FOR VACCINA TRAINED BLIDE 3	NM_016440	<u> </u>

	C2200	
archaracterized procedularius content (1002)	AF246240	<u> </u>
Si cara	8(004542	7
uncharactarizad bone marrore protein 8M039	AX023669	1.34
DMA segment on chromosoms 12 (unique) 2.489 ezpressed sequence	NN_007360	7.
Commensus includes do.N742553 FELATEST DB XREF = 4:5110841 DB XREF = 4:17455402.21 KLONE=1946E.256995 AUG=19, 184592 protein kinase, bysine deficient 1 FL=40-MM O1 A742553	b:NM_01 A/2553	
Consensus includes gb:WB4525 /FEA=EST /DB_XREF = gi-1395637 /DB_XREF = est:x490g09;s1 /KLONE=INAE:356800 /M6=Hs,7949 DKF2P58682420 protein	W64525	1.34
neutral sphingomywiknase (N-SMase) activation associated factor	NM_003580	7.
C6F42 protain	NM_016035	1.34
2. S-digoademylate symbotise 2 (69.71 kD)	NM_016817	<u>*</u>
uggerd uggerd	086862	<u>.</u>
Inpodenced protein 1 (J.Z.195	NM_022/58	<u>.</u>
Charles are grown	A6011158	
MATTOROGO OF MICHON BITTER BY CONTINUE IN 11-1	ABUSUMOS	<u>.</u>
Gortein-coupled receptor 43	NH 005306	1 7
ordin herein chechistas, receipt has a cohnection (PTRR) interaction contein (linein) sloke i	AA 1952 S9	7.
Comments in the Control of the Contr	85052059	2
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homboo of rat nachin	NN 018054	6
larrio	NH 005573	ñ
small GTP-binding protein	NM 030981	1,33
amploid beta procursor protein binding protein 1, 5940	NH 003905	133
general braschbion factor IIIA	NM_002097	1.33
homblog of mouse qualing QND (KN domain RNA binding protein)	AF142418	1.33
caldum channel, voltage-dependent, gamma subumit 2	AL022313	1.33
plateled derived growth factor (NN_016205	1.33
photophoribosyl pyrophosphate synthetuse_associated protein 2	HM_002767	1.33
stronal artigan 1	N126490	1.33
RAW0737 gene product	8£783632	1.33
Lat Cot must fermin	NM_002343	1.3
SASSA Protein	80001123	£.
ALL STATES AND ALL ST	8(004998	3 :
2 unad Bucan Arri	NM_U0626/	3 :
manufacture of the second seco	NK ODOKS	6.5
Fancer anests, complementation evens 6	NH 004629	=
ribosomal protein 1.9	NM_000661	1.33
dones 23667 and 23775 zinc finger protein	BC000330	1.33
glycoarytehosphaiddyfinoaitha specific phospholipuse 01	AL031230	1.33
destin (actin depolymenting factor)	NH_006870	9 :
the same and deposit of the same of the sa	MM_004078	3 :
The state of the s	04332	£
provinces, (1) profilement) manifolding for including the control of the control	NW OTCOME	9 5
efform-schräde frotein fanse 2	A762811	3 5
neches pare complex interacting protein	AC002045	1.33
ademykáta bánane 2	AU154985	1.33
Consentus incidas go. NO22458 1 (DEF Erformo supiens CDNA FL1239) fis, clone MAMMA1002769, weakly similar to Homo supiens cell cycle progression restoration 8 protein (CPR8) mRN MO22459	8) mRt AXO22459	£.
NAU SALSE K. A. A. I.	85674658	E :
temposouri posouri i securi i	56421186	3 :
Art process in the state of the	TCRES.	5.5
TAR DAY Inches protein	NM 007375	9
DVCZP4100199 protein	AL080129	2
serologically defined colon cancer antigen 3	NH_006643	1.33
branched chain keto acid dehydrogensse E1, beta pohypcpide (maple syrup unne disease)	HSSS78	1.33
hypothetical protein FU13868	NM_022744	1.33
SWGMF related, matrix essectated, actin dependent regulator of chromatin, subhamity a, member 2	NM_003070	E
MCIVe mencharmosome mentinance deficient 6 (AlSS homolog, 5, pombe) (5, cerevisies)	NM_005915	E :
I AT THE CONTROL OF BUILDING AND STATE OF THE CONTROL OF THE CONTR	ACOMENTS.	3 :
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	and the product of a constant and the constitution of the constitution of the constant of the	9777777	
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	The terrorism of the proper legislation and the proper legislation and the property of the pro	46136603	2
	The control of the co	(OCC21 A)	3 :
	COMMISSION DESCRIPTIONS SAPERS MINK, CURA UP-COSON, 150 (TOM CORE UN-COSON, 150), ITEX=MINK /UB_ARCH=03-104-MS-12, (1032), HORD SAPERS MINK, CURA UP-COSON, 150), ITEX=MINK /UB_ARCH=03-14, INC. = 03-14, INC. = 03-	MR ALUANDIA	3 5
	RAVI, GIYEA activiting protein I	NM_002885	.33
	protein tyranine phosphatese, receptor type, N	NN_002846	-33
	zinc finger protein 36, (3H type-like 2	U07802	<u></u>
	Abox binding protein 1	NM_005080	1,33
	Proofbettal protein FU10734	NW 018197	1.33
	Consumers included the Manne series of TSH canner for natural ATP canner from natural ATP canner for natural ATP c	isis 41295618	133
	According to the state of the s	NA 015084	
	CUVA parameter and the country of th	toscio TV	3 :
	GONN_CO2913.1 /GEF Enomo sapens repication (activator () i (145kD) (RFC1), mRNA. /FEA=mRNA /GEN=RFC1 /PROD=repication lactor ((activator 1) 1 (145kD) /08_ARF =	EF = NM_002913	1.33
	copine M (neuronal)	AB009288	1,33
	Williams-bearn syndrome chromosome region 1	NM_022170	1.33
	cohomore DNA directed my	AK023002	1 33
	The state of the s	PC000313	:
	7 avit-translati	21/00019	.33
	eudit (nucleatide diphosphate linked moiety X) type motif 2	NH_001161	1.33
	IQM1624 protein	AX024651	1.33
	Ill and when Ill	MW 001106	=
	an additional action	80.00	3
	math homolog 1, colon carker, nonpolyposis type 2 (E. col.)	NM_000249	-33
	baror protein, translationally controlled 1	A188178	1,33
	om 21 US suffice 100 tel contain	AF026402	133
	The second of th	NA 003646	: :
	dil primi indicata di nata	Mr Wish	3
	QAA070 protein	AL136821	1.33
	(QX15 homolog, cytochrome c aziemby protein (yeast)	NM_004376	1,32
	dwomosome 8 open reading frame 2	190773	1.32
	contrativ	AJ 578583	2:
	CONTRACTOR OF THE PROPERTY OF	NA DOLOSE	1
	- ASPART MARKATAN ASPART	9791007	7.
	regulation of nonsense transcripts	029323	× :
	IDAN 149 protein	N64681	1.32
	opiaid growth factor receptor	AF 172452	1.32
	NTE crotain	NN 014015	132
	The continues associated BMs hinding recently like t	NH 003252	:
	No. 19 Court A management of the control of the con	30300 VV	7 6
	UNIVERSAL DE LA CAMBRIA DE LA	NH_03050	3 :
	usod Dame	NA_030601	7 :
	protocolinen UK	NH_017675	2
	Korkhoud bas H.	NM_003923	27
	Consumus includes gis. 4472139 /FEA=EST /08_XREF=gi:4334229 /08_XREF=est:436a:10.x1 //LONE=1MAGE:2148378 /UG=Hs.9683 Unal (Hsp40) homolog, subfamity C, member 3	A472139	1.32
	hypothetical protein FU22427	BF129339	1.32
	Sedenosyflomorysteine hydrotae-like 1	AA479488	1.32
	Sec23-interacting protein p125	AK021846	1,32
	nather bore combes interaction orders	AA308853	2
	The state of the s	46167438	4 5
	Company Compan	A-16/436	7
	d-containing 7 (Ivrn)	NM_022168	1.32
	hypothetical protein	NM_015702	1.32
	protein tyrosine phosphatase, non-receptor type 2	AJ828880	1.32
	mulate detrydrogenase 2. W.O (mitochondrial)	ALS20774	27.
	IGAAGO14 gave product	NM_014665	1.32
	pyroette dehydrogenzae (iposenide) beta	AL117618	1.32
	mitochandrial ribosomal protein 518A	AB049952	1.32
	protein phosphatase 3 (formerly 28), catalytic subunit, alpha isoform (cakineurin A alpha)	AL353950	1,32
	6-enventarizations in smithse	M97655	2
	official condition of the state	79725114	2
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ansnoadpate-e-maldehyde dehydrogenase-phosphopantetheinyl transferase	AF151057	
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immunoglobulin (CD79A) binding protein 1	NM_001551	7.1
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mannershalong betwee protesse c	A8008047	7.1
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HSW034 protein	AL031427	Ξ.
hypothetical protein FUE3027	AAS24500	1.1
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, nuclear pore complet protein	NM_020401	Ξ.
proliferation-associated 264, 3840	U87954	1.1
zinc finger protein 189	NH_003452	1.1
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neuron-specifik protein	80001745	1.1
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collagen, type VI, alpha 1	A141603	Ξ
ungictensin I converting enzyme (peptidyl-dipeptiduse A) 1	AI623989	Ξ.
estralacin 2	AX024064	1.1
Ftst homolog 3 (E. coli)	NM_017647	Ξ.
hypothetical protein MGC11138	A675178	Ξ
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glutamate nich WD repeat protein GRWD	861500 MM	=
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hypothetical protein FU10902	A8007930	Ξ
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chromosome 22 open reading frame 4	NH 002244	Ξ
patassium inneardy-rectifying channel, subfamily 1, inhibitor 1	11 13 15 BE	==
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hypothetical protein FU12949	NA_023008	5 5
sarrodykan, beta (43k0 dystrophin-essociated glycoprotem)	995670	<u>;</u> ;
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reversion-inducing-cysteine-rich protein with hazal motifs	MVC2837	: :
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hypothetical protein FU20694	KM_01/928	5 3
eukayvotic translation indistion factor 3, subunit 10 (theta. 150/170kD)	A123320	Ξ:
serine (or cysteine) proteinase inhibitor, clade B (oxalbumin), member 7	NH_003784	Ξ:
ELAV (endryonic lethal, abnormal vision, Drosophila)-like I (Hu antigen R)	B(U033/6	3 :
AAD blood group (transferase A. alpha 1-3-N-acetykadactosaminyttransferase; transferase B. alpha 1-3-gadactosyitransferase)	NM_020469	Ξ:
enclain drauffde somernae netated protein (calcium-binding protein, intestinal-related)	8(006344	5
hypothetical protein FU22-402	NH_024608	= :
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NH_01847 NH_06385 NH3555 NH3555 NH35555 NH25555 NH25555 NH_05550 NH_05550 NH_05550 NH_025182	dual specificity phosphatase 2	NH_004418	6.1
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hypothetical protein	BF572868	<u>s</u>
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1 003 protein	NM_020232	8
SAT (sea determining region 1) -box 22	NM_006943	8.
Wisbatt-Makish syndrome protein interacting protein	KM_003387	60.1
putatable 28 kDs protein	HM_020143	6.1
Invasification protein FLI21562	NM_025113	1.09
Procedural protein FL2332	NM_024955	5.3
density-resoluted protein	AB014731	1.09
dendorin suffice orderdycan (Namera)	A373676	1.09
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(61-02 protein	W249752	S
bided to IAZF1	8F382924	8
BH-protocacherin (brain-heart)	NH_002589	8
Diseage syndrome critical region gene 6 like	AA631156	8
hypothetical protein FLI10057	NM_017984	<u>8</u>
KDM.111 protein	AW249934	8
WADH dehydrogenese (ubiquinone) 1 beta subcomplex, 4 (15kD, 815)	NA_804547	8
active GCR-related gene	119704	<u>s</u>
RNA polymerze I 16 kDe subuni	NM_015972	8
galactose-4-epimerse, UDP.	AL031295	S :
hypotherizal protein FU23441	NM_0246/8	<u> </u>
Sp2 trenscripton factor	028368	5 5
Metangeneous nuclear nbonucleoprotein H3 (2H9)	KM_021644	S 8
CDID antigen, d polypeptide	MM_001766	8 . 9
Conserves includes gb:\(ACE3384 \nabla Feminan DNA sequence from clone \(6)\(K)\(1\) on chromosome \(64\), \(.24.3\). Contains the \(H)\(CF\) (Schnum-2) gene for \(H)\(Y)\(P)\) \(F = Human DNA sequence from clone \(6)\) \(K)\(F)\) in \(H)\(H)\(H)\(H)\(H)\(H)\(H)\(H)\(H)\(H)	1 ALUC3584	<u> </u>
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establish Descriptions	BC000419	8
000792446022 motion	KM 014044	8.
hypothetical protein FU20260	AF323729	1.09
engulfment and cell motility 2 (ced-12 homolog, C. elegans)	NN_022086	69.
H1 histone family, member 2	BC002649	 8
ets varient gene 5 (ets -relatind molecule)	X76184	1.09
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mitogen-activated protein kinase 7	57/570	5 5
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ubiquitin-certulating enzyme £20 2 (UBC4/5 homolog, yeas!)	KM_003339	1.09
O22 articles (1944)	KM_006139	1.09
ref finger protein 2	NM_005798	60,1
regulatory factor X, 1 (influences HLA class II expression)	NM_002918	87
interlacon-related developmental regulator 1	AA747426	8
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GAVZZ77175. I (DEF #Home supients PNAS-138 mRNA, complete cds. (FEA=mRNA, PR0D=PNAS-138 (DB_XREF=gi:12751080 (MG=Hs.326790 Home supients PNAS-138 mRNA, complete cd. AZZ77175	ate cc AF277175	8.3
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dual-aperificity tyrosine-(17)-phosphorylation regulated kinase 2	Y09216	8.
nadia metaloprotainase 14 (membrane-inserted)	X83535	8:
hypothetical protein MGC2574	NM_024098	8
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hypothetical protein FU22761	NM_025130	60:
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core-binding factor, nert domain, alpha subunit 2; translocated to, 1; cyclin D-related	X79990
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calcium/calmodaliin-dependent serine protein kinase (MAGUK tamily)	NM_003688
hypothetical protein FU00002	AK024446
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ubiquitin-conjugating enzyme E2D 2 (UBC 4/5 homolog, yeast)	BE621259
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merofichorin 2 (biddenii ecoustic neuroma)	AF122827
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2 anal woodware 473	NH_004091
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hypothetical protein FU20241	NH 017721
hypothetical protein FU11730	NM 022756
pro-platelet bask protein (includes platelet bask protein, beta-thromboglobulin, connective tissue-activating peptide III. neutrophil-activating peptide: 2)	R64130
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reset tentomere protein angens (1550k)	NM_020238	80.
And Administration of the Control of	AB045369	3
NAME OF THE PROPERTY OF THE PR	043949	3
Proposed powers to 10 to 20	NH_018025	8
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bie and Compyrie A. emino and N-explicansferies (gydne N-chologitransferies)	NM_001701	1.08
6CL2/adenovins E18 19th interacting protein 2	BC002461	1.08
hypothetical protein FU12567	NM_024714	1.08
immunogodulim kapa variabe 1-13	AW408194	8
unquitin specific protease 4 (prote-oncogene)	AJ346043	1.08
introgen activated protein kinase (inase)	AA780381	1.08
Enchange protein 91 (KFF7, HTF10)	NH_003430	1.08
Landers and Lander	AX022548	1.08
gyceronephosphate O-ecyltharsterase	NM_014236	1.08
binor protein, translationally-controlled 1	ALS65449	1.08
perine racemase	NM_021947	1.08
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fatty-acid-Contyme A ligase, long-chain 3	089053	1.08
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2 operation in the second control of the sec	AC005070	8
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Propublical protein FLL25609	NH 022072	8
mycain, light polypeptide 4, alkali; atrial, embryonic	152005	80
caterin (catherin-associated protein), alpha-like 1	MN 003798	80
protein kinase D2	AF309082	\$0,1
ufamin	AF120274	8
hypothetical protein FU22643	NM_024635	80.1
polymense (DNA directed), gamma 2, accessory subunit	NH_007215	1.08
innunoglobulin superfamily, member 4	NH_014333	80.1
hypothetizal protein MGC2550	NM_024071	1.08
ICANOS S) protein	AV699744	1.08 80.1
CONDESSION AT \$20 NEA=EST /08_XREF=9:11009351 /08_XREF=est:AU147830 /CLONE=HAMMA1001818 /U6=Hs. 296713 Homo supiens CONA FLIZ295 fs., clone NAMM AU147830	MAMM AU147830	8.
softe (arreit family 2) (organic annon transporter), member 3	AF085224	1.08
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putable L-type neutral amino axid transporter	AU154782	80.1
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at 10 months and promise 1. The control of the cont	A-280094	8 :
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endodamic reticulum axidomaturin 1-lbeta	100 MM	8 8
6 protein-coupled receptor 44	AF118265	3 3
redinaic and receptor, alpha	191506	80.
hopern withe (glucosanine) 3-0-sufforms lease 301	NM_006041	1.08
Talk binding protein 1	NM_006788	1.08
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county surfusions sector 1 (macroprings)	M37435	20.

interhaction 9 receptor	NN 002186	ă
bstyrophilin, subtamity 2, member A2	KM 006995	8
The Instrumentation excepts (editor-related protein)	NH_012410	8.
Proceeding protein DE C2-XVI 158 similar to widely -interspaced zinc finger moits	A828531	1.08
DATIONAL MODES BOALD 1497 / FEDERAL 1703 / FEDERAL 1703 - MILE - SELVIN 13497 / TONE FIRST FOR FORE 137308 MRNA, PARTIAL COST. TONE FIRST FORE 137308 MRNA, PARTIAL COST. TONE FIRST FORE 137308 MRNA, PARTIAL COST. TONE FIRST FIRS	AU134977	8.
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transfer or FRR 1	AW071795	5 .
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Mypothetical protein FLIZ167	NH_005694	80.1
Mypothetical protein FU12707	AA401703	80.
solute carrier family 7, (cationic arrino acid transporter, y+ system) member 11	/90720 V	80.
hypothetical protein PR00899	Abutua/3	8 8
O site of albumin promoter (albumin D-box) binding protein	COCO10_PM	3 3
hypothetical protein	0/9663	9.5
hypothetical protein FU20030	0/0520_MA	6
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IGM0345 pratein	AAAAA3ES	9 5
ditydrokiposmide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup unine disease)	M27093	5 5
activin A receptor, type 18	WM 020328	9 5
poly (A) -specific ribonuclease (deadenylation nuclease)	NM 002582	3 5
Consensus includes gb:JA205593 /FEA=EST //DB_JREF==g11803601 //DB_JREF==g118058-005-s1 /KIONE=IMAGE-646762 /LIG=Hs 26837 Homes animals and many nictor sector of a standard of a standar	A4206583	9.5
hypothetical protein DIGI2564D0478	10m A4203393	6.5
ubiquitin specific protease § (isopeptidase T)	Macadan	6.5
decayhypusine symbase	101500 101) 5
pertial transcript encompassing TMC211630 gene	VAC 10_114	ò. :
6 protein-coupled receptor kinase-interactor 1	0/00100/	1.07
H-44 antigan	NM_014030	1.07
apostosis inhibitor 5	X91103	1.07
Proodhetical protein H6(3)62	AF229253	1.07
Whose acid recessible protein	278349	1.07
Outside Incl. 1992/08:1944felds at Norm contents and Allowan India and an arrange of the succession of	NM_016167	1.07
Parisforming growth factor beta-activated bisses-binding review 1.	N92708	1.07
major histocomostibility cometa. class II. 100 less	NM_006116	1.07
Prophetical protein EU1 4639	NM_002120	1.07
Consensus includes op: III74494 /FEA=EST /OB XRFF=ai 1384781 /OB XRFF=ai -ad78110 at /AT INEFE 1245A7 AT INEFE	A88462/	1.07
Consensus includes go.AW979196 FELEST (78, XRE Engl 3170444 / 78, XRE Engl 5170444 / 78, XRE Engl 517044 / 78, XRE Engl 51704 / 7	W/4494	1.07
hypothetial protein FU23393	CO AW9/9196	6.
thructecticle repeat containing 11 (TMR-essociated protein, 230 kDa subunit)	MM_UC4039	, i.o.
nuclear protein, statis-tolangiectusia locus	2025	6.
V+41 arythroblastosis virus £26 oncogene honalog (favian)	U03643	9.5
potossium channel, substamily K, member 10 (TREK.2)	MT_003236	6.5
immunoplobulin kappa constant	46103674	6.5
NDCMA18' protein	44160181	è :
hypothetical protein FU11467	WW 024963	<u> </u>
hypothetical protein FU20123	175710 MM	3 5
Consensus includes gb./L.109705.1 /OEF = Homo supiens mRNA full length insert CONA clone EURO(NAGE 73332, /FEA=mRNA /OB .XREF=@;569834 /NE=Hs,9997 Homo supiens mRNA full 109705.	M. 109705	9 6
chondratin suffice protection (bunkan)	AF020043	60.
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remainment receipture (street)	NM_016083	1.07
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IDANO237 men product	SY AM071454	1.07
protein phosphase 2. noutator subunit 8 (856), delta inform	60003103	1.07
ATP-6TP-binding protein	KM_006245	6.07
podymense (RNA) II (DNA divected) polypeptide 8 (140k.D)	MM_UUG631	6.6
IDA1067 protein	A802890	9 5
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tratted to the state of the sta	249258	
holocarboaytes synthetese (biotin-(proprionyl-Coenzyne A-carboxylase (ATP-hydrolysing)) ligase)	NM_000411	
tumor necrosis factor receptor superfamily, member 10b	AF016266	
weside-associated membrane protein 3 (celtubrevin)	BC003570	
hypothetical protein FU23209	NM_024895	
endathelin receptor type A	251545	
RAMOA'I game product	6610/203	
(nt 90) [nt studential studenti	MM_013084	
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45, ribasonal profession (X7) softram	NM_015920	
Languages ab AL137784 (DEF = Human DNA sequence from clone RP 1-19913 on chromosome 6 Contains ES1s., STSs, GSSs and CpG islands. Contains part of the gene for a novel pro AL137784	el pro AL 137784	
wefres/broame tinese 17a (apoptosis-inducing)	AW194730	
witngen-activated protein kinase 11	US3442	
hypothetical protein McCoOK	NM_024345	
poweronicous portycas con me	72459	
definite (company)	A763123	
M domain certaining 2, with 2Mf domain	A681013	
Apatrophin (muscular dystrophy, Ouchenne and Becker types), includes 0X5142, 0X5164, 0X5206, 0X5230, 0X5289, 0X5268, 0X5270, 0X5272	NM_004010	
shosphatidic acid phosphatase type 2(AF047760	
artosine dehydrogenuse	A:04/004	
arkouping profess. ? Information (arrier)	113852	
Changaint and a state of the contract of the c	A735639	
(6)-Op protein	NM_015936	
top90-easociating relative of (dk.)?	NM_017913	
UATA, member RAS ancegane family	AF112206	
Tatherican (PELS) marker medicin 1	U34074	
sentance from the promotion is settler factor	M60718	
prophotophatiae	NM_006903	
gkdamske receptor, ionotrophie, AMPA 3	NM_007325	
protein kinase (binding protein 1	A8032951	
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auther receipt subtanist 3 crub (, member)	X03348	
nancyte to meruphage differentiation-essociated	NM_012329	
QAN1059 protein	AK022610	
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unitaride-sensitive cation channel 3, testis	NM_020322	

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zinc finger protein 220	MM_006766	1.07
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Improductal protein FU20085	MM_017660	1.07
CONTROL OF THE STATE OF THE STA	NM_D05692	1.07
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hypothetical protein FU20259	8(000978	1.07
H-ectropalactosaminidase, alpha-	M38083	1.07
paly (A) binding protein, cytoplasmic 3	NH_030979	1.07
CLY changing provien rags	NM_016656	1.07
NEW PROTECTION OF THE PROTECTI	222551	6.0
A/O homeo (), pombe	NW 004584	60.
nitris caide synthase 2A (inducible, hepatocytes)	124553	1.07
solute carrier tarrity 25 (carritine/asy/carritine translocase), member 20	BC001689	1.07
disposition of anticological CTATS	KM_018393	1.07
protein hyrashe phosphatae, non-receptor hipe substrate	D86043	6
tragle & mental retardation, autosomal homolog 1	86025078	1.07
zinc finger RHA binding protein	A459274	1.07
Amplifying in the defences a Clevernile, Chromosome region, candidate 3	AV705253	1.07
ripporture prount LLL. displactors samified seasons	NA_01/61/	6.6
Moort syndrom, mental retardation, middae hypoplasia and elliptocytosis chromosomal region, gene 1	AK023637	0.
souts caries family 25 (mitochondrial center, Araba), member 12	NM_003705	1.07
CQT Constraint () homotog underlanden (yest)	AF032900	8.
indicate a captus consistent of the consistent o	MM 004977	<u> </u>
M-deacmytaes/N-suitotransferrae (hepuran glucosaminy) 1	NN 001543	8
gb:L2136. I OBF=Homo sepiens acute myeloid teutemia associated protein (AMLIEAP) mRINA, complete cds. FEA=mRIN /GEN=AMLIEAP (DB_XREF=gi+00340 /FL=gb:L21756.)	21756	1.08
glaumen huteotote banding protein (e protein), garnna / intaktoen? ************************************	BF432795	8 8
sin-Lessockide polypeptide, 300	AF055993	8 8
spandylospidyysad dysplasia, late, pseudogene	AF291676	90.1
translocase of outer mitochondrial membrane 70 homolog A (yeast)	80003633	1.06
injentation [characteristics and the control of the	AL137749	9.
Specialistis (Freety)	MM_0020/6	8 2
RAMPING game product	A304674	8 8
interfaction 10 meroptor, alpha	NM_001558	8.
hypothetical protein	NM_017571	8.
hypothetical protein FU11722	NM_024970	9.1

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TA1 cytotoxic grande-associated RNA binding protein	H96X9	
hypothetical protein FU13593	NN_024780	8
endothelist cell growth factor 1 (platelet-derived)	NA_001953	8.
andidonate 12-ipoxygenize pseudogene 2	AF020774	8.
RAB11A, member RAS oncogene family	NM_004663	-8
smell inducible cytakine subtamily 8 (tys-X-tys), member 11	AF030514	8
Gmethylarginine Gmethylaminchydrolase 2	AK026191	8.
Consensus includes gis AU1146809 /FEA=EST /DB_XREF=gi: 11008330 /DB_XREF=est: AU146809 /CLONE=HEMBB1001564 /UG=Hs. 287476 Homo supiens cDNA FU12004 fs, clone HEMBB	mo sapiens cONA FU12004 fis, clone HEMBB AU146809	9.
CA2+-dependent activator protein for secretion	NH_003716	1.06
cathain 13. H-cathain (hear)	NH_001257	1.06
triancite motif-containing 3	A419307	9.1
anneared and fermions of the area descent	BYUGUU MM	8
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porting nearn 10	778510_MN	3 :
ring finger protein 1	NM_002931	8.
hypothetical protein FU23119	NM_024652	8
ganna-aninobutyric acid (GABA) A receptor, gamna 3	69/20%	8.
membrane-bound transcription factor protease, site 2	1884_0_MN	8
stornatin (EBP72)-like 1	NM_004809	1.06
novel protein	NM_017515	8.
anexin A7	NH_004034	8:
hypothetical protein FU23445	NM_025075	1.06
8-call (LL/Amphoma 11A (zinc finger protein)	AF080216	90.1
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mypoprecial protein FU20116	1/9/10 HM	8 1
popaje protein 3		8
Consensus includes gp.ALT38761 (DEF #Human DNA sequence from clone RPT1-16H23 on chromosome 10. Contains the gene KIAN0204 (HSLK) for a protein kinase, the COLTAR gene for		8
nuclear receptor coactivator 2	AI040324	8.
thrombopoietin (myelopraliferative leukemia vinus oncogene ligand, megakaryocyte growth and development factor)	U59495	8
nedealar protein AVIT	NM_018454	8.
coactivator-associated arginine methyltransferase-1	M551784	8
mysloid/lymphoid or mised-lineage leukemia (trithoras homolog, Drosophila); translocated to, 2	671221	90.1
interferon, garma-inducible protein 16	80256677	8.
papidylprolyl isomerse (cydophilin) kite 2	NM_014337	90.1
Consensus includes ab/N995896 /FEA.EST // 08 XRF = al. 3434872 // 08 XRF = est ab 21402 x 1 // (AIE = HAGE 1696890 // 05 = Hs. 301463 Human Chromosome 16 & A.C. clone (179875K-A.E. Al. 095898	in Chromosome 16 8AC clone CIT987SK-A-6 AIO95896	1.06
ADDS1 - dia 3 (S. cerevisia)	AB016223	1.06
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7 FFF-1 200 OB100	C20120_MM	3
protein triate, CATP-dependent, regulatory, type II, alpha	/SIMO NA 00415/	8
IPSS larget gene i	A8007457	96.
WUTZIN 3	964900 MN	<u>.</u>
IAM binding protein 17	NM 022897	2
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(QA1115 protein	NM_0004/5	8 8
lamin 8 receptor	MW A0330C	8 8
ATPase, H+ transporting hysosomal (vectodur proton pump), member H	4E077614	8 8
appropriatesaminiduse	HC4073	8 8
heat shock 70t0 protein 4	4404334	8 3
high-glucose-regulated protein 8	95550	8 3
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FRICKERS (Section Frame)	AK023924	8.
reponence present Held 179	NM_024340	90.1
Nephrokations overspressed gene	NM 002514	26
weide-usociated membrane protein 1 (synaptobrovin 1)	AU150319	8
carbonypaptidasa D	085390	ž
F-box and WD-40 domain protein 18	900000	3 3
dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	C#369630	<u> </u>
DG7295446522 zerdein	49CF00	8
solute carrier family 16 (monocarboxylix acid transporters), member 5	ALCHOM43	8 3
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EGZ/adenovirus E18 1960 interacting protein 1		2
transforming growth factor, beta 1	_	3 3
Consensus includes gb:X84340.1 /DEFEM sapiens mRNA for lg light chain, variable region (ID/CIL001VL). // FEAEmBNA /GENEID V) gene // PRODE immunoclobusin light chain, variable region		3 2
antificasis, prograssive homolog (mouse)		3 3
bridging integration 1	/+0610_PM	8 3
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private dividenment lines investigate	7/9510	8
MANDELSKE alpha class (A member 2	NM_002610	8
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candidate tumor suppressor p33 lMC I homolog	9001300	9 9
UP (aucine-rich repeats and PD2) and no PD2 protein	Med (40)	<u> </u>
decambenduses Hite 2	M 001314	8 3
similar to hypothetical protein MND-2336	*/*!OC.P/	8 3
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candidate turns automated. 1818 the homeless the control of the co	AMM/ AW166925	8.
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Consensus includes ob-86233999 AFEA=857 AFE 2865 - A-17240776 AFE 1885 - A-174408AD - A-MILLONDE-MARCELA ARCHARACTER ARCHARACT	NM_003322	8.
ADP-riboratefan fater-file 1	67665799	90.
polymerase (RNA) II (DNA directed) polymerase (133.0)	9915104	8
100%2000 EXIDENCE TO THE PROPERTY OF THE PROPE	19/761	8
ELADOR TOTAL	NW_014043	8
Elif frank market	NM 014949	8
Paradhadra medical (19240)	KM_006763	8
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service with research to the content of the content	NM_001042	8.
Professional designation of the control of the cont	NM_007352	90.
ALL'S TREALMENT FOR CHEN GITTERWINDELEGAN I DOMINING (3) POINTING	AIS67462	8.
and another particular another	X83412	8
Consuments Includes gb: AL 122122. 1 (DEF = Namo sapiens mRNA; CDNA DNE 2p4341.098 (from clone DNZ2p434.098). IFEA=mRNA (DB_XREF=gi:6102949 / NG=HS.2274559 Homo sapiens mR AL 122122.	1 mf AL122122	8
(UMOS) protein	AB023147	9.7
IQAOS 22 protein	A052003	97.
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IQA40239 protein	NM_015288	1.03
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ubaquitan-conjugating enzy me EZA (RAD6 homolog)	NM_003336	-03
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hypothetical protein Ny014	BF939727	1.03
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EDISCONT WELCH PROCESS	719100 NN	60.
non-metastatic cells 3, protein expressed in	AL031718	1.03
SCAN domain-containing 1	AL 109965	1.03
hypothetical protein FU12903	NM 022753	5.0
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инториодал	AS63393	1.02
advenencyc, alpha-10-, receptor	M76446	5.
CONSONIAL INCLODES DO: WASBAR TEA=EST 708_XREF=gi 1337022 708_XREF=estrze44a09.s1 /CLONE=IMAGE:325144 /UG=Hs,285814 sprouty (Orosophils) homolog 4 /FL=gb.AZ227517.	olog 4 /FL=gb:AF227517. W48843	1.02
metanome antigen, tamihy 8, 1	NM_002363	3.
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MTMAN nucleoprotein (des moyakin)	BG287862	2.03
rypothetical protein FU12455	NM_022078	3.
SWISMS related, matrix essociated, actin dependent regulator of chromatin, subfamily a-like 1	NA 014140	1.02
QAMOOS protein	45275044	5
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# FIRST AND A COLUMN TO THE PROPERTY OF THE PR	NM_013383	7.02
HIV-I Kev Binding protein	A742626	29.
IQAA0150 protein	D63484	-0.0
breast cancer 1, early onset	NM 007295	1.02
protein phosphatase 1, regulatory (inhibitor) subunit 8	NH 002713	201
monthetical protein FIL23SB4	NA 024588	2
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	zinc finger protein 198	NW 003453	2
	paptidas 0	NH 000285	2
	hypothetical protein MGC5297	NM_024091	29.1
	Consensus includes gb-XW969913 /FEA=EST /08_XREF=gi:8159757 /08_XREF=ext:EST381991 /NG=Hb.105121 ESTs	AW969913	1,02
	hypothetical protein FU10233	NM_018034	<u>3</u> .
	dystrophia myctonica-protein kinase	M87313	<u>5</u>
	nedesphosmin (nuclealer phosphopratein 823, numetrin)	A191576	20.1
	spiriong factor 30, suburnit 4, 49k0	60004273	3.0
	nbosonal protein (1)	AL049597	3.
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	72 Designatory normal analysis	AA083478	7.02
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	be a control of the c	NA_004129	3
	Magnetic of Springs 1	NM_003835	3
	Should also a should be sh	NM_014864	26.
	under Control	AL049923	1.02
	Variable charge, A chromosome	AF167079	<u>3</u>
	nuclear receptor subtamily 4, group A, member 1	NM_002135	3
	ILMO/81 protein	AB018324	1.02
	inflagam-attivated protein kinase kinase kinase linase I	W744529	1.02
-	DIG ZP 564692 protein	NM_015601	5.
	m/tochandrial ribosomal protein L20	NM_017971	70.1
	makanoma antigan, family 8, 3	NM_002365	7.0
	serine (or cysteine) proteinase inhibitor, clade 8 (ovalbumin), member 2	NM 002575	1.02
	chaperonin containing TCP1, subunit 6A (zeta 1)	8£737030	1.02
	hypothetical protein MGC 11335	NN 030819	9
	v-jus sartoma vivis 17 occopere homolog (avian)	KF17172	5
	subtotansterse family, extensive traffering member 2	100 MI	2
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	reproducement produced to the substantial (CDLD)	NM_024/55	20.5
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	hroothetical protein FU1222	000710 WA	ž 3
	instalin promoter factor 1, homeodomain transcription factor	130329	3 6
	Obished mannose beta I.2-N-acetylglucosaminyttransferase	PLCC IO NA	9
	PDZ domain protein (Drosophila insD-titus)	96.2500 MM	<u> </u>
	Noner, neuronal immediate sarly gene, 3	NA 004838	9
	purine-rich element binding protein A	NM 005859	9
	hypobecical protein FU20533	BC002745	201
	DV2.P566183 protein	8002888	1,02
	methionine adenosytransferase II, alpha	8001686	8
	(GLAZ protein	NM_016026	20.1
	13 upot	A671049	20.1
	Impoduces protein PUIS6	NM_025138	20.1
	Lethwedded, the horning of J (Unsophila)	NN_004423	20.1
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243 GPs-4-ACTIVATING PROTEIN	A1040009
Consensus includes gb:XF234255.1 (DEF=Homo sepiens clone KM36 immunoglobulin light chain variable negion mRNA, partial cds. FEA=mRNA /PR00=immunoglobulin light chain variable W234255	e AF234255
hypothetical protein FU23336	NH_024671
sylochrone classes subunit VII.a polypeptide 2 (liver)	NM_001865
Paptodytaraty isomerae (cytochilin) like 2	037220
consumers includes go.XMM9/0344 /F.EA=EST /08_XREF=gi:8160789 /08_XREF=est:EST383027 /J06=Hs.291839 ESTs	AW970944
solule camer tamity 16 (manocarbosytic ecid transporters), member 3	NM_004207
Euthrophinis, subtansiy 3, member Al	U90552
Elekany, member 3	A1765445
hypothetical protein FU12505	NM 024749
putative UDF-Gal/Mc;polypeptide N-acetylgalactosaminyltransferase T9	BE906572
stands alpha and HEAT/Armadillo motif protein, ortholog of Drosophiia	A1927797
paricentricles material 1	41924817
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IGM1616 protein	10000
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bactericidal/permeability-increasing profession	191083
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C NAME OF THE PROPERTY OF THE	AA457021
F protein 10 (NDA 1)	X52332
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	M336631
	MM_005508
	NA_018391
f. branches (6 commission)	NH_016076
	NM_003170
	NH_016349
mad to S-AZACTORINE induced gene 2	NM_022461
	NM_001268
g protein-the ?	8000296
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xr. SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein 1)	M982754
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M /DEF=Homo suprens chromosome 19, BAC 273239 (CIT-8-320613) /FEA=CDS /DB ,XREF=qi-4559317 /UG=Hs, 284229 Homo saniens chromosome 19 BL	C007204
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Consensus includes qb.M798R23 FEA=EST / 08 . XREF =q; 5564295 / 08 . XREF = est: we3b05.st / (LONE=IHMGE2348625 / UG=Hs, 1050 pieckstrin homoloon; Sec) and collected domains 1 M798R23	1 A798623	8.
hypothetical protein FU20568	NM_017885	5.
glucoseminyt (N-ucetyl) transferase 1, core 2 (beta-1,6-N-ucetylglucosaminytteansferase)	NM_001490	3
(61:50 protein	AL589866	8
desings stimulation factor, 3' pre-RNA, subunit 1, SOKD	L02547	3.
cold inductible RNA binding protein	NM_001280	2
6TF21 repeat domain-containing 1	NM_016328	2
cerad-lipotuscinosis, neuronal S	A911687	3
gbit14456.1 /DEF Human Ig rearranged mu-chain gene V.N.O.H.i-region, complete cds. /FEA=mRNA /DB_XREF=gi:398497 /FL=gbit14456.1	114456	1.02
Enc. finger protein 262	AAS21508	20
KQAQ210 gene product	A654161	3.
hypothatical protein FU11101	NM_018322	1.02
IQAA0378 protein	238645	3.
eristaless-like homeoba: 4	NM_021926	1.02
(QAOS5) protein	A633851	1.02
panoratitis-usociated protein	NM_002580	3.
Consumsus includes gb-XV097640 /FEA=EST //08_XREF =gi:3445898 //08_XREF =est:qb59±08.x1 //LONE=!MAGE:1704374 //u6=Hs.66187 Homo sapiens clone 23700 mRNA sequence	A097640	2.0
RADS1 hamalog (Reck hamalog, E. culi) (S. cerevisiae)	014134	3
hypothetical protein LOC55565	NM_017530	3
transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	A992187	20.
WI-casociated protein 3	AL031709	9
intracistemal A particle-promoted polypeptide	NH 005897	20
jagod I (Nagile syndrome)	U73936	70
Shydroxybytanine (serotonin) receptor 10	NN 000864	70
Consensus includes gb:AX021690.1 /DEF = Home supers cDNA FU11628 fs, close HEHBA1004238, /FEA=mRNA /DB XREF = qi:10432926 /UE=Hs. 306610 Home supers cDNA FU11628 fs.		20
KDAA0377 protein	BF002844	20
netin 1	NM_004822	3
aint finger protein 219	NM_016423	20.7
IGAA0599 protein	A1738980	2
hypothetical protein DKZLp4341037	NM_030952	1.02
2 unascal burburg (MAS)	NM_006824	3
(05-7)vd and section and secti	NH_003438	8
Interest connected to the control of	AL121749	2
Procedures F11320	AK024262	3 3
tumor necrosis factor receptor superfamily, member 1A	NN 001065	=
KH-type splicing negulatory protein (FUSE binding protein 2)	NM 003685	5
CD3D amigen, dekla pokypaptide (TIT3 complex)	NH_000732	<u>5</u>
U6 snRW-esociated Smille protein	80005938	<u>5</u>
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Conservation of the Law of more than the Conservation of the Conservation of the Law of	747.41.035297	5
ettal sequence (mammay tumor and squamous cell carrinoma-associated (p80/85 src substrate)	NN 005231	5
neuropeptide FF-unide peptide precursor	NM_003717	10.1
AU RNA binding protein/enoyl-Coenzyme A hydratase	NM_001698	5
inclear domain 10 protein	60004130	<u>5</u>
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(1.00 ft) gene product	AIS39425	1.0
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IUB1 budding uninhibited by benzimidazotes 1 homoloo beta (vesst)	NH 001211	5
blepharophimosi, epicaribus investus and ptosis, candidate	N 021812	5 5
MGG1.1 protein	AB016900	5
(GL-2) protein	NM_015957	1.0
activin A receptor, type II	NH_001616	1.0
ribosomal protein L37	BF216701	<u>1.</u>

malanocortin 3 receptor	NA_019888
Yaophospholipase I	PG288007
phosphorytase kinase, beta	NH_000293
suppressor of polassium transport defect 3	N655698
discussion-like pertition 1 receptor	101157
polassium voltase-sated channel, shaker-mained subfamily, beta member 2	AF044253
activi, alpha 2, smooth musde, aorta	MA_001613
POU domain, class 5, transcription factor 1	AF268613
Vensforming growth factor beta-stimulated protein TSC-22	AK027071
ymadophysis-like protein	15/900 NN
6-protein coupled receptor SALPR: somatestatin and annotensin-like preside receptor	NM_016568
dathim, light tehrenológ (Lz.)	NM 001833
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INICIAET TRESTOR CO-TRIPESSOR	0/687/0
general transcription latter III, polypeption (Jajpin subunit, Sokii)	LICEUD_NN
naces transcription lactor 1, alpha	AL031//8
suppressor of 5. certaisiee gcr2	NM_007265
tumor necrosis factor receptor superfamily, member 5	NH_001250
LM domain-containing preferred translocation partner in liponu	AL044018
DNA segment, numerous copies, expressed probes (GS1 gene)	KM_012080
RQA0470 gane product	W126789
chaineagic receptor, nicatinic, alpha potypeptide 4	NH_000744
uppressor of K+ transport defect 1	AF195514
heuropathy target extense	NM_006702
NAP-timase activating death domain	AB002356
- willing the	80004300
SCL2-antagonist/biller 1	KM_001188
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hypothetical professional profe	86167522
Additional 16, RDF cacherin	NH_004062
Chromosonia 2 open reading frame 2	KM_019063
weuthough (rill) homolog	NM_004647
CONSTRUCTION OF DESCRIPTION OF THE STATE OF THE STATE	
syladirame P450, subfamily ills (phenobachital-inducible), potypopilde 6	NM_000767
hypothetical protein FU10385	NM_018081
iki homalog 1 (Drosophila)	AB011537
chromosome 22 open reading frame 2	NM_015373
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	hypothetical protein FU12886	NA_019108	-
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ribosomal protein 511	22.06
ribosomal protein, large P.2	15.91
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syntretase (1.5, -n, -5 represent transcript regions 5 prime, modile, and 3 prime respectively)	2.57
	5.53
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Consensus includes gb:8973387 /FEA=EST /DB_XREF=gi:12340602 /DB_XREF=est:60224235351 /CLONE=IMAGE:4330861 /UG=Hs.305989 Human DNA sequence from clone RP3-483K BF973387	3.69
M 10038 Human 185 KINA sequence, length 1969 bases, middle target bases 647-1292	3.69
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90:22331 I /OEF = N septens protein tyrosine kinase gene, complete (DS / FEA=mRNA / PROD=protein tyrosine kinase / DB_XREF = git 405/52 / FL = git.225437.1	3.63
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with DNA methylment in the proving of the province of the prov	To file Fermon supients mit NA, CDM DNZpA34H054 (from clone DNZp434H054), FEA=mit NA, DB_XREF=gi.526.26.22 /UG=H1,274517 Homo supients manages agring unite disease) ranisacytes (E2 component of branched chain lacto acid dehydrogenase complex: mapte syrup unite disease) PSX 1 /DEF=Homo supients mit NA, CDM DNZpA34H054 (from clone DNZpA34H054), FEA=mit NA, DB_XREF=gi.7018527 /UG=H1,22483 Homo supients mit NA, CDM DNZpA32H007) And (lg), short basic domain, secreted, (sernaphorin) 3A (edigizzarin) 1 /DEF=Homo supients mit NA, CDM DNZpA351 (from clone DNZpA3817 ESTs, Weakly similar to ALUI_HUMAN ALU SUBFAMILY I SEQUENCE CONTAIN 1 /DEF=Homo supients mit NA, CDM DNZpA354 (from clone DNZpA38F1622), FEA=mit NA, DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050998 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. EET /DB_XREF=gi.8050999 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. A. EET /DB_XREF=gi.8050999 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. A. EET /DB_XREF=gi.8050999 (NG=Hs, 287658 Homo supients CDNA, FUZ1305 fs, d. A. A. A. EET /DB_XREF=gi.8050999 (NG=Hs, 287658 Homo supients CDNA, FUZ13049 fs, clone THYROLOGO865, FEA=mRNA, DB_XREF=gi:04035992 /NG=Hs, 181810 Homo supients CDNA, FUZ13049 fs, clone THYROLOGO865, FEA=mRNA, DB_XREF=gi:04035992 /NG=Hs, 181810 Homo supients CDNA, FUZ13049 fs, clone THYROLOGO865, FEA=mRNA, DB_XREF=gi:04035992 /NG=Hs, 181810 Homo supients CDNA, FUZ13049 fs, clone THYROLOGO865, FEA=mRNA, DB_XREF=gi:04035992 /NG=Hs, 181810 Homo supients CDNA, FUZ13049 fs, clone THYROLOGO865, FEA=mRNA, DB_XREF=gi:04035992 /NG=Hs, 181	Months F. Acros Supplied (American transported) mamber 6	MM_U00638
ress includes gizkL080160.1 // DEE=None sapients mRNk. c/DN DNE2p434NOS4). // FEA=mRNk. // DB_MEE=gizbEasez // Use=Hs. 274517 Home sapients mRNk. c/DN DNE2p434NOS4). // FEA=mRNk. // DB_MEE=gizbEasez // Use=Hs. 274517 Home sapients mRNk. c/DN DNE2p434NOS4). // FEA=mRNk. // DB_MEE=gizbEasez // Use=Hs. 274517 Home sapients mRNk. c/DN DNE2p43207 (from clone DNE2p762N127). // FEA=mRNk. // DB_MEE=gizD18527 // Use=Hs. 22453 Home sapients mRNk. c/DN DNE2p43207 (from clone DNE2p762N127). // FEA=mRNk. // DB_MEE=gizD18527 // Use=Hs. 22453 Home sapients mRNk. c/DN DNE2p43207 (from clone DNE2p762N127). // FEA=mRNk. // DB_MEE=gizD18527 // Use=Hs. 22453 Home sapients mRNk. c/DN DNE2p43207 (from clone DNE2p762N127). // FEA=mRNk. // DB_MEE=gizD18527 // Use=Hs. 22453 Home sapients mRNk. c/DN DNE2p43207 (from clone DNE2p43207 (from cl	1.0EF=Homo supiens nRNA: cDNA DNZ2p324H054 (from clone DNZ2p324H054), FEA=mRNA DB_XREF=gi:SE62622 AlG=Hs,274517 Homo supiens m mana-sylase (EX corporent of branched chain keto acid dehydrogensae complex; maple syrup urine disease) FSK 1.0EF=Homo supiens nRNA: cDNA DNZ2p762H127 (from clone DNZ2p762H127), FEA=mRNA DB_XREF=gi:7018527 AlG=Hs,22483 Homo supiens nRNA: nain (4g). short basic domain, secreted. (semaphorin) 3A [6] [6] [6] [6] [6] [7] [7] [6] [6] [7] [7] [7] [7] [7] [7] [7] [7] [7] [7	the receiver the second of the	VBOZOSS)
religoantide branched chain transacytes (E2 component of branched chain beto acid dehydrogenase complex; maple 97mp urine disease) 40,2015 defected containing protein 2 40,2015 defected containing protein 2 41,2016 dehydrogenase complex; make 517.04 bit 120,444 10E = Hermo sapiens mik 11,5144 41,2016 dehydrogenase complex; make 517.04 bit 120,444 10E = Hermo sapiens mik 1,5144 10E = Hermo sapiens mikk cibk bit 1,5145 10E = Hermo sapiens cibk 1,5144 10E = Hermo sapiens mikk cibk bit 1,5145 10E = Hermo sapiens cibk 1,5145 10E = Hermo sapiens cibk 1,5145 10E = Hermo sapiens mikk cibk bit 1,5	rentarylate (EZ component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) staining portein 2 rentarylate (EZ component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) staining portein 2 rentarylate (III) staining portein 3 rentarylate (III) rentarylate (IIII) rentarylate (IIII) rentarylate (IIII) ren	nsus includes ob. 4,080160 1 /0EF = Homo sapiens mRNA: CONA DIVEZD434H054 (from clone DIVEZD434H054). /FEA = mRN	
arming, wide colled-coll containing protein 2 AP 220132 AP 22013	tabing pratein 2 PSK In Off = Homo supiens mRIA, CDNA DNS DNS DREAD (from clone DNS DATA) (FEA = mRIA / DB _NEE = 9;7018527 / NG = Hs, 22.483 Home supiens mR (19), short basis domain, secreted, (semaphorin) 3.4 (edgizzarin) (edgizzarin) (edgizzarin) (fEA = EST / DB _NEE = 9;8166019 / DB _NEE = est EST 386921 / NG = Hs, 283517 ESTs, Weakly similar to ALUI _HUHAN ALU SUBFAMILY I SEQUENCE CONTAIN OF PPP B (edgizzarin) (edgizzar	olipounide branched chain transacriase (E2 component of branched chain keto acid dehydrogenase complex: manle syrup	
to derived STEQUIts binase PSK HI JOIST HI JOOSS HI JOSS	PSX 1. DEF = Homo supiens mRNV. cDNA DNE2p762H127 (from clone DNE2p762H127). FEA=mRNA DB_JREF=gi:7018527 /UG=Hi.22483 Homo supiens mRNV. cDNA DNE2p762H127 (from clone DNE2p762H127). FEA=mRNA DB_JREF=gi:7018527 /UG=Hi.22483 Homo supiens mRNV. cDNA DNE2p762H127 (from clone DNE2p288F162F). Weakly similar to AUTI_HUHAN AUT SUBFANILY I SEQUENCE CONTAINOR, STREF=gi:8166019 /DB_JREF=gi:8166019 /DB_JREF=gi:10437382 /UG=Hi.287658 Homo supiens cDNA. FU21305 fis, clone (COLO212A. /FEA=mRNA /DB_JREF=gi:10437382 /UG=Hi.287658 Homo supiens cDNA. FU21305 fis, clone (COLO212A. /FEA=mRNA /DB_JREF=gi:10437382 /UG=Hi.287658 Homo supiens cDNA. FU21305 fis, clone (COLO212A. /FEA=mRNA /DB_JREF=gi:10437382 /UG=Hi.287658 Homo supiens cDNA. FU21305 fis, clone puccessory of the contained of the color puccessory of the color puccessor of the color puccessor of the color puccessory of	orming, acidic coiled-coil containing protein 2	
nous includes go.AL 157484 I OEF Elsomo supiens mRNA; CDNA DNG 2p/82P1127 (from clone DNG 2p/82P1127). FEAF = mRNA / DB, DREF = g;7018S27 / MG = Hs, 22483 Homo supiens mRNA; CDNA DNG 2p/82P127). FEAF = mRNA / DB, DREF = g;7018S27 / MG = Hs, 22483 Homo supiens mRNA; CDNA DNG 2p/82P2 / MG = Hs, 2845172 / MG = Hs, 2845192 / MG = HR, 200552 / MG = Hs, 2845192 / MG = HR, 200552 / MG = Hs, 2845192 / MG = HR, 200552 / MG = Hs, 2845192 / MG = HR, 200552 / MG = Hs, 284517 / MG = Hs, 2	1 (DEF = Homo supiens mRNA. CDNA DNZ.PG.EATI27 (Trom clone DNZ.PG.EATI27), FEA.= mRNA /DB_JREF = gi:7018527 /NG=H1, 22483 Homo supiens mB hair (bg), short basic domain, secreted, (semaphorin) 3A (equivariant) (adjezamin) (adjezamin) (bef = Homo supiens cDNA. FUZ1305 fs, clone (C0L0212A, FEA.= mRNA /DB_JREF = gi:10437382 /NG=H1, 287558 Homo supiens cDNA. FUZ1305 fs, ch. CNTA / CONTA /	te derived STE20-like kinase PSK	
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rome c caidate subwait Vb	FEA=EST (DB_AREF=gi-8166019 / DB_AREF=ert:EST386921 / AUG=Hs.283517 ESTs. Weakly, similar to AUU1_HUHAN ALU SUBFANILY I SEQUENCE CONTAINED. The IB In Contained to August a sequence of the COLO2124. FEA=mBNA / ALS AREF=gi-10437382 / AUG=Hs.287658 Home sapiens cDNA: FLZ1305 fs., cl. Color supplements cDNA: CDNA (ACT4) ALS AREF=gi-10437382 / AUG=Hs.287658 Home sapiens cDNA: FLZ1305 fs., cl. Color supplements cDNA: CDNA (ACT4) ALS AREF=gi-10437382 / AUG=Hs.287658 Home sapiens cDNA: FLZ1305 fs., cl. Color PLACET / ALS AREF=gi-10437382 / AUG=Hs.287658 Home sapiens cDNA: FLZ1305 fs., cl. Color PLACET / AUG France August / AUG France Augus / AUG France AUG	Cakium binding protein A11 (calgizzarin)	02920 MN
NW_005755 The farm vira induced gene 3 The farm vira induced gene 3 The induced gene 3 The farm vira induced gene 3 The induced gene 4 The induced general gene 4 The induced gener	TEA=EST (DB_AREF=gi:8166019 (DB_AREF=er:EST386921 / JUG=Hs.283517 ESTs, Weakly similar to AUU_HUMAN ALU SUBFAMILY I SEQUENCE CONTAINOR. Type IB In n In n In DEF=Homo supiens CDNA: FILZ1305 fs, clone COLO212A. FEA=mBNA (DB_AREF=gi:10437382 / JuG=Hs.287658 Homo supiens CDNA: FILZ1305 fs, cl. (ABF=BRAND) ABFET (ABFE-BRAND) ABFET (ABFET)	rome c andase subunit Vo	AIS57312
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0.035073 Mr. Quidesta protein receptor, type IB Mr. Quidesta Mr. Quid	no. Npe 18 In DEF = Homo supiens CDNA. FUZ1305 fs. clone (COLOZ124. /FEA=mRNA /DB_XREF=gi:10437382 /UG=Hs.287658 Homo supiens cDNA. FUZ1305 fs, ch. In DEF = Homo supiens mRNA; CDNA DGFD566F1622 (from clone DKTD588F1622), /FEA=mRNA /DB_XREF=gi:8807308 /UG=Hs.278435 Homo supiens mRNA; CDNA DGFD586F1622 (from clone DKTD484F1126), /FEA=mRNA /DB_XREF=gi:8807308 /UG=Hs.378455 Homo supiens mRNA; CDNA DGFD43441126 (from clone DKTD43441126), /FEA=mRNA /DB_XREF=gi:8807308 /UG=Hs.378455 Homo supiens cDNA FU113845 fs, chone THYRO1000865, /FEA=mRNA /DB_XREF=gi:10435992 /UG=Hs.181810 Homo supiens cDNA FU113849 fs, chone THYRO1000865, /FEA=mRNA /DB_XREF=gi:10435992 /UG=Hs.181810 Homo supiens cDNA FU113849 fs	nsus includes gb.AW974816 /FEA=EST /DB_XREF=gi:8166019 /DB_XREF=est:EST386921 /UG=Hs.283517 ESTs, Weakly	Wilar to ALU1_HUMAN ALU SUBFAMILY I SEQUENCE CONTALAW974816
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In the contents with contents and contents of the contents of	In 176F = Homo sapiens CDNV: FLIZ 1305 fs, clone COLOZ 124. FEL=mBNA /DB_XREF=gi:10437382 /UG=Hs_287658 Homo sapiens cDNV: FLIZ 1305 fs, d. FOR = Homo sapiens mBNV. cDNA OVZ p586F 1622 (from clone DNZ p586F 1622). FEL=mBNA /DB_XREF=gi:5817120 /UG=Hs_2789435 Homo sapiens A=EST /DB_XREF=gi:789822 /DB_XREF= est;NP14c03 r/ TLOME=UMAE: 135460 /UG=Hs_28686 Homo sapiens cDNA FLI 1022 fs, chone PUNZ 10337 /DEF=Homo sapiens cDNA FLI 1320 /UG=Hs_306455 Homo sapiens Freceptor, alpha, 5 alpha, low-affinity (granulocyte-macrophage) CEF=Homo sapiens cDNA FLI 13849 fs, chone THYRO 1000865. FER=mRNA /DB_XREF=gi:10435992 /UG=Hs_181810 Homo sapiens cDNA FLI 13849 fs.	retical protein FUZ1032	NM_024906
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usu includes gb.AL 10201 I / OFE =Homo sapiens MRM; CNU D0275565 FG22 (from close D0725486F FG22) / FEB=mRM / OB_ARFF=gi:5817120 / UG=Hs. 278435 Homo sapiens AL 110201 usu includes gb.AL 10201 i / OFE=Homo sapiens AL 110201 musu includes gb.AL 10204 FEB=gi:5817120 / UG=Hs. 278435 Homo sapiens AL 113238 Gm usu includes gb.AL 10205 i / OFE=Homo sapiens AL 13378 Gm usu includes gb.AL 10205 i / OFE=Homo sapiens MRM; CNM D0725434K1126 (from close D0725434K1126). FEA=mRM / DB_ARFF=gi:5807998 / UG=Hs. 306455 Homo sapiens AL 13378 Gm usu includes gb.AL 13389 Gm usu usu usu usu usu usu usu usu usu us	/ OBE = None supient mRN, CDN 01/2/256f 1622 (from clone 10/7/2586f 1622). /FGL=mRNA /DB_2/8EF=gi:5817120 /Ui=Hz.278435 None supiens A=EST /DB_2/8EF=gi:789822 /DB_2/8EF=estyh74-c03.r1 /CLONE=INAGE.135460 /Ui=Hz.288681 Home supiens cONA FULI 1022 fst, done PLACE 10037 /DBE = None supiens cONA FULI 1022 fst, done FUACE 103460 /Ui=Hz.288681 Home supiens cONA FULI 1022 fst, done PLACE 10037 /DBE = None supiens cONA FULI 3849 fst, done THYRO 1000865. /FEA=mRNA /DB_2/8EF=gi:10435992 /Ui=Hz.181810 Home supiens cONA FULI 3849 fs	poratein L. 2	
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edical protein FU23185 **Laminating receptor, alpha 5 Bi5665183 L23349 L23349 MM_004608 NM_004608 NM_004608 NM_007039111 / DEFEHorno susiens, CDAN FU13849 fix, close FHYRE I 13849 fix, close FHXE I 13840 fix, c	receptor, alpha 5 , alpha, low-affinity (granulocyte-macrophage) DEF=Homo sapiens cDUA FUI 3849 fs, clone THYRO1000865. /FEA=mRNA /DB_XREF=gi:10435992 /UG=Hs, 181810 Homo sapiens cDNA FUI 3849 fr	etical protein	690610 MN
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nden spin indedes ab-XW23911.1 /0EF-Homo saziens; CDA, FU.13849 fis, close FHYRO1000865, FEA=mRNA //B. XRFF=ai:10435992 /Mi=Ht. 181310 Homo custerns //DNA FI113849 fix, ARX 33911.	/DEF=Homo sapiens cDNA FU13849 fis, clone THYRO1000865. /FEA=mRNA /DB_XREF=gi:10455992 /JG=Hs,181810 Homo sapiens cDNA FU13849 fi	stoyltransferase 2	NM_004808
395 includes de: AUC 3911.1 / DEF = Home sapiens CDA FUL 3849 fis, clone 1H/R01000865. /FEA= mRNA /DB XREF = 0::10435992 /JG=Hs 181810 Home sapiens CDNA FIL13849 6 AK023911	345 induces go:Mu23911.1 /U£t = Homo sapiens CDNA FU13849 fis, clone 1H7R01000865. /FEA=mRNA /DB_XREf = gi:10435992 /UG=Hs. 181810 Homo sapiens CDNA FU13849 fi AND23911	roden	NM_007003
The second secon		isus includes gb.M023911.1 /DEF=Homo sapiens cONA FU13849 fis, clone THYR01000865. /FEA=mRNA /DB_XREF≂gi:1	35992 /JG=Hs.181810 Homo sapiens cDNA FLJ13849 fi AK023911
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gb/NM_Q24305.1 /DEF=Homa sepiens hypathetical pratein HGC(4278 (MGC(4278), mRNA. /FEA=mRNA /GEN=MGC(4278 /PR00=hypathetical pratein MGC(4278 /NB_XREF=gi:13236535 /NG: NH_Q24305			

rypothetical protein MGC2474	
hypothetical protein FU21477	CE 1630 MM
polymerase (DNA directed), eta	מיטייייייייייייייייייייייייייייייייייי
CONSENSUS INCHORES DAIN 126492 / FEA=EST /OB_XREF = gi.3595006 /OB_XREF = est; qd82h06.x1 / KLONE=IMAGE:1736027 /UG=Hs. 104258 Homo sapiens MRNA eson 1. 2, 3, 4, clone:RES MICEASY	HEIREY AT COASC
consensus includes gi)8(005365.1 (DEF =Nomo sapiens, chone IMAGE:3829438, mRNA, partial cds. /FEA=mRNA /PR00=Unknown (protein for IMAGE:3829438) //08_XREF=gi:13229199 // B(005365	3199 A 80005365
odymense (RNA) II (DNA directed) potypopitide B (140M)	AW770896
AMP responsive element binding protein-like 1	025696
neuropeptióe Y neceptor 16 (pseudogene)	US9431
Pezolúnsse 2	AI761561
Okster Incl. A1949010:wq36a07.11 Homo sapiens cDNA, 3 end ktone=IMAGE-2473332 ktone_end=3 /gb=A1949010 /gi=5741320 /ug=Hs. 104036 Aen=457	A949010
mananabiding lectin serine protease 1 (C4/C2 activating component of Ra-reactive factor)	8C000587
V/3-domain GR02-like 3	AF036269
thymid hormone receptor interactor 11	8(002656
hypothetical protein PR02849	NM_022335
decay accelerating factor for complement (CDSs, Gromer blood group system)	80001288
mitogen-activated protein kinase kinase 5	071088
colactor required for Sp1 transcriptional activation, subunit 2 (150kD)	AX023368
phosphaticylinosital 4-kinase, catalytic, beta podypeptide	081802
HF-binding transcription factor Dianglei	Alcuesed
Puppersion of Immorgenity 6, prostate (RZ leukocyte antigen, antigen detected by monoclonal and antibody (M4))	NW 030881
MODIFICATION AND ADMINISTRATION OF THE PROPERTY OF THE PROPERT	NM 002886
V. E., DETTOEL OI I.O. OKCOGNET ANNUT	8F966878
DIAMATON consistence intransice of gainstan, in	AB007941
societies dependencesse (IVADP+) soluble	NM_005896
(Continue of the continue of t	AK023668
VIP-binding casette, sub-family 0 (ALD), member 3	NM_002858
usukayotic translation initiation factor SA	AA393940
ghycophorin E	NM_002102
ntenis protein	NM_022487
inhibin, beta (NW_005538
reversion-inducing cysteine-rich protein with kazal motifs	AK022897
Consumus includes gb:AU147017 /FEA=ES1 /08_XREF=gg:11008538 /08_XREF=est:AU147017 /KLONE=HEMBB1002132 /08=HS:301303 Homo saprens curva FU144080 HS; done numb on Anna Landa August Augus	ACMOD AUI 4/01/
Moderates it level	NM 017964
Physical December 100007 MG H 200007 MG H 2000007 MG H 200007 MG H	iens mf A1049260
CONSTRUCTOR SPACE CONTROL THE PROPERTY OF THE	1 fis. d AK025724
condition force V (moscelerin lable factor)	NM_000130
ine frace crotein ?	NM_007212
AITPes, Class I, type 88, member 1	86252666
homeo box A10	Al375919
(ansensus includes gb.160435831 / DEF =Homo sepiens clone ASMneg1-b3 immunoglobulin lambda chain VI region, (1GL) mRNA, parisi cds. /FEA=mRNA /GEN=1GL /PROD=immunoglobuli NaDA3583	oglobul AF043583
indexis protein 6	NM_003/8/
macrophage stimulating, pseudogene 9	0C0033
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teneral indicates granted from the control of the c	104162
conservats includes op 143504. I (DEF Human unidentified mRNA, partial sequence, FEA=mRNA, DB, XBEF=q;1171236 AUG=Hs, 159901 Human unidentified mRNA, partial sequence	rce U43604
prostate differentiation factor	
K034S3 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	X03453
protein kinase, OMP-dependent, regulatory, type II, alpha	8(002763
hypothetical protein FU10534	AK026565
Consensus includes gb.AW574933 /FEA=EST /08_XREF=gi:7246472 /08_XREF=est:UI-HF-810_abg-b-09-0-UI.s1 /CLONE=IMAGE:3057353 /UG=Hs.248844 ESTs, Wealdy similar to ALU1_h MW574933	ALU1_1 AW574933
hene growth factor receptor (TNFR superfamily, member 16)	/0250/ A4100157
2 uridomeus	AK537887
erforecyte membrane protein band / 2. (stomatin)	115894
Comment includes the MADOSARY I TOFF EHOMO stations, CDNA. EL12784.0 fir, chore KMAA2709 FFEAE. EL049366 (JG=Hs.287293 Homo stations cDNA. EL12284.0 fis, ct AGOSARY) fis. clc AX026493
Inferrogeneous nuclear ribonucleopratein H1 (H)	AV753392
odoucia 2 (beta)	NM_017482
ine finan rintein 16 (errorssed in lestis)	FC/CW
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dimethylar	dinethylarinine dinethylarinohydrolase	4) 078459	777
PRO0644 protein	potein	NM_014136	*
cost protei	cost protein gamma-cop	NM_016128	2.43
Consensus	consonsus includes gb:186403790 /FEA=EST /DB_XREF=gi:13297238 /DB_XREF=est:602419627F1 /(LONE=IMAGE:4826599 /UG=Hs. 158154 ESTs	BG403790	2.43
mop ewes	soma domain, immunoglobulin domain (1g), short basic domain, secreted. (semaphorin) 3C	NM_006379	2.43
CDP-Gal:be	UDP-Galbetak NAc beta 1,3-galactosyttransferase, pohypeptide 5	NM_006057	2.42
hypothetic	γγραthetical protein FLI20059	NM_017644	2,42
OCI4 cell	DC14 cell dirision cycle 14 homolog A (5. cerensiae)	NM_003672	2.41
hypothetic	typothetical protein FLL23548	NM_024590	2.41
hypothetic	rypothetical protein FUZ2558	NH_022747	2.41
nuclear factor I/B	tter UB	U70862	2,40
hypothetic	vypothetical protein My014	NM_030918	2.40
hypothetic	ypothetical protein FU20006	NM_017618	2.40
WNT1 indo	MMT inducible signaling pathway protein 3	AF143679	2,40
dictalant he	ácticopt homalog 2 (Aenopus taevis)	NM_014421	2.39
Consensus	consensus includes gb:AV021440.1 /0EF=Homo sapiens cDNA FU11378 fis, clone HEMBA1000456. /FEA=mRNA //B XREF=qi:10432625 /UG=Hs:6937 hypothetical protein FU10276	AX021440	5.39
(onsensus	Consonsus includes go.N.359578.1 (DEF = Homo sapiens mRNX; cDNA DIEZDS47N163) (FEA = mRNA DB XREF = cis 8655637 (ME = Hs. 306511 Homo sapiens on AL359578	m AL359578	2.39
(onsensus	Consensus includes gb: AM629050 /FEA=EST / DB_XREF = gi:2541437 / DB_XREF = est: zu84406.s1 / CLONE=IMAGE: 744658 / UG=Hs. 50760 ESTs, Highly similar to BimL H. sapiens	AA629050	2.39
Dystonia m	Dystonia musculorum of mouse, human homotog of	AL049215	2.39
Consensus	Conservas includes ab A 13177.1 (DEF = Homo stations 2506) mRNA sequence IF 6A=mRNA / DB XXEF = 01-4406602 (UG=Hs. 183475 Homo stations 2506) mRNA sequence		2 30
hypothetic	Thropothetical protein FU22746		33
H1 histone	histone family, member 4	AI 253759	
unc-51-file	me. 5. like kinase 2 (C. elecant)	1000000	200
anc finacr	the floor protein 42 (invelople sector relinate and, reconstitution)	A1732248	2. 6
chechoont	thectooni superess of	44860806	2.5
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(A. I) O niecko	(1.4)	V4C23AV	£3,
	Additional property of the control o	A0038403	/° '
Factor and a second	ende talley, cylosodd, i'w prende prenering, member 3	5/25/2	75.7
		X75208	2.37
Cranonacia	t usual state over other parties and the state of the sta	085939	5.36
unoudom.	Labophorn (gp.115, leukosalin, Ud43)	X60502	5.36
Consensus	consensus includes 90:K00627.1 /DEF =thuman kpni repeat mma (cdna clone pcd-kpni-8), 3 end. /FEA=mRNA /DB_XREF=gi:337653 /UG=Hs.203776 Human kpni repeat mma (cdna clone K00627 Consensation K0062	1 K00627	5.36
Consensus	COTSONIAS STATES OF A VIOLE FOR SEA FOR FULL 1983 FS, CLORE HEMBB1001337, FEA=MRIA (DB_XREF=g:10433364 /UG=Hs,193162 Homo sequiens CDNA FULL1983 1 AXQ22Q45	1 AX022045	2.36
hypothetica	rypothetical protein FU20097	NH_017667	2.36
(onsensus	COTAGNIANS BENDAMEN BY 1862 FEA=EST /OB_XREF = gi:273899 /OB_XREF = est:EST01755 /CLONE=HHCPNGO /UG=H5.314534 ESTs, Moderately similar to ALUS_HUMAN ALU SUBFANILY S M78162	S M78162	2.35
hypothetica	hypothetical protein FU20019	NM_017624	2.35
calcium/cali	akium/calmoddiin-dependent serine protein kinase (MAGUK family)	AB039327	2.35
M 10098 Hu	M10098 Human 185 rRMA gene, complete [_SM3 represent transcript regions 5 prime. Middle, and 3 prime respectively.	H10098	2.35
Consensus	consensus includes gb:580491.1 /DEF=stem cell factor (alternatively spliced) human, preimplantation embryos, blastocysts, mRNA Partial. 180 nt. /FEA=mRNA /GEN=stem cell factor. SE 580491	\$80491	2.35
hemoglobin	hemoglobin, gamma 6	NH 000184	2.34
transcription	Transcription factor 20 (AR1)	119345	2.34
Consensus	CONSENSUS Includes CO. MCC23783.1 (DEF = Homo saniens cDNA FILI 3721 fis clone PLACE/2000450 (FFA=mBNA IDR XRFE=ni 1045620 AIG=Hc 289035 Homo saniens cDNA FILI 3721 fis atto32783	4K023783	72.
(61-58 protein	en e	NM O16006	7.
hypothetical	hypothetical protein FU10254	NM 018041	7.
interleutin 1	interletatin 1 receptor antagonist	BES63442	2.33
Bloom syndrome	rone		2.33
Consensus	CONSTRUCTION OF THE STANDARD SEA FEATER TOB XREF = estaction of the STANDE STANDARD S		2.33
in missappod	polazisum inwardty-rocitiying channel, sublamity I, member 8	NM_004982	2.33
hypothetical	hypothetical protein FU14310	NM_025028	2.33
Drombospondin	ugu l	NH_003246	2.33
Calmodutin	amoduin (prosphorylate lunase, defla)	M27319	2:32
M (ODG) M:	Municoff infinitely documents receptor, substantly 6 furth IM and IIII domains), in member 3	AF009643	2.32
honothetical	Three-training to time sequence, tengin 1909 beats, 5 printe (alger bases 1259-1936) Proofficial products (1914-2)	M10098	2.32
IGAA0304 ov	ilprovide dese produit de la constant de la constan	NM_024825	25.2
a disintentin	institute of productions domain 17 filmore marrait factor slabs, commedian annual.	A-1052/9	2:32
Ser (ser de	(See address) to the control of the	KM_003183	2.32
phosphatidy	phosophaticylinosistic 4-phosophate S-lineare type III alpha	NM_005030	7.7
homeo bos (8	83	NM 022658	2.36
(GI-86 protein	-	BC000637	2
guanine nucl	guarine nucleotide binding protein 13, gamma	NN 016541	
potassium v	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	NH 002252	231
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CONTRACTOR MICHAEL AND	AF229163
consensus includes gb.AW 451711 /FEA=EST /08_XREF = gi:6992487 /08_XREF = est:UI-H-613-ale<-02-0-UI.s1 /XLONE=IMAGE:2736386 /U6=Hs.313760 ESTs	AW451711
COTSOURD STANDSOOA3 IFELEST (DB_XREF =gi:6047387 /DB_XREF =eti:2001:05:11 /LIONE=IRAGE:2592488 /UG=H1:326464 Homo sapiens (DNA: FUZ1702 fs, done (OLO9 ANOSOO43	7L09. AW090043
staf homotog 1 (E. cali)	NM_018696
coegulation factor II (thrombin) receptor	766100 WH
Consensus includes gb.XXXXX1448, I / DEF = Home supiers CDNA FU10586 fs, clone MTZRP2003986, /FEA=mRNA /DB_XREF=9:70227 3 /UG=15,301255 Home supiers CDNA FU10586 fis XXXXII +448	6 hs AX001448
DING 11541.1 (DEF Home supers hypothetical protein PR02832 (PR02832) miNA. (FEA=miNA.) AEH=PR02832 (PR02832 PR02832 (PR02832 (PR02832 PR02832 (PR02832 (PR02832 PR02832 (PR02832 PR02832 PR02832 (PR02832 PR02832 PR02832 PR02832 PR02832 PR02832 (PR02832 PR02832 PR0	14C01074
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Towards by December 1000720 1 (Aff #Human FST clone 251800 mainter transcend Heman's sequence. FEA.=mRNA /DB 28EF = 01:2921608 AUG = 15:42192 Human EST clone 25:1800 mail 1807700) ma U80770
the first of the medium representations of the second seco	NM 006090
documents related 0.4	NM 000797
cholimersk revestor, nicotinik, alpha pohypestide 3	M37981
7A trocaine lineae	AW276646
myt myekocytomatosis viral oncogene homotog 2 (enian)	NH_005377
(UA/093) protein	NM_014950
gistamete receptor, metabotropic 8	AV236922
rypotherical protein FU13769	NM_025012
LADS4, S. cerevisiae, homolog at, B	NM_012415
GDMF family recentor alpha I	NM_005264
consensus includes abs/393960 /FEA=EST //08 XREF == 4223507 //08 XREF == 11004.41 //LONE=IMAGE:2108455 //JG=Hs.274851 ESTs	A1393960
consensus includes th AW970881 IFEA=EST (0) XREF==0:8160726 (0) XREF==s1EST382964 (AIG=Hs, 205660 ESTs	AW970881
conservas includes ab AL 137590.1 (DEF EHOMO suciers MRNA, cDNA DIG EA4340610 (Hom clone DNZ 2434K0610). FEA=mRNA /DB. 2REF =q; 6808330 /U6=Hs, 300785 Homo sapiens	iens AL137590
ymphocyte cytosotis protein 2 (SNZ domain-containing leukocyte protein of 76kD)	AJ123251
ignal transduction protein (SH3 containing)	AB001467
adenomatasis polyposis (di	\$67788
PR00097 protein	NM_014114
IAAB 34, member RAS oncogene family	AF 133588
programmers activator and CANL interactor	NM_012452
Consonaus includes ga.X702306 /FEA=ES1 /08_XREF =gi:10718636 /08_XREF =as:A7702306 /(LONE=A0881005 /M6=Hs.321211 ESTs, Highly similar 10 zinc finger protein 216 splice vi A7702306	ce v: AV702306
H3 histone family, member (NM_003531
hypothetical protein FU12975	NM_024809
hypothetical protein FU14346	
Consensus includes gb:AL117451.1 /DEF = Homo sapiens mRNA; cDNA DK72p586E2317 (from clone DK72p586E2317). FEA=mRNA /DB. XREF=gi:5911901 /UG=Hs.293563 Homo sapiens	-
poptide TY, 2 (seminalplasmin)	NM_021093
(D34 artigen	M81104
mediti metalloproteinase 25	NM_022718
binaction (Valnesin receptor)	8F589024
W(3) protein	NM_025258
veuronal cell adhesion molecule	NM_005010
VAX transcription activation domain interacting protein 1 like	AI357401
rypothetical protain FU13162	NM_025002
CONSONSIN INFORMATION OF THE STIT ON BUTTLE FOR COASSONS TO BUTTLE COASSONS TO THE COASSONS AND COASSONS TO ST	AW173720
INA-binding protein gene with multiple spliking	084109
Consensus includes gb.AV726900 /FEA=EST /08_XEF=gi:10836321 /08_XEF=est:AV726900 /FLONE=HTCABD05 /VIG=Hs.7000 ESTs	AV726900
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dhymotrypain ((addecrin)	NM_007272
associated gamma adaptin ear containing, ARF binding protein 2	
	A799984

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ATPase, Ca++ transporting, plasma membrane 2	R52647
dromosome 4 open reading frame 5	AY013295
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Conservate includes gb:XXQ25194.1 /DEF = Homo supiens cDNA: FU21541 fis, clone CQL06166. FEA=mRNA /DB_XREF=gi:10437657 /UG=Hs. 306784 Homo supiens cDNA: FU21541 fis, clone CQL06166.	ns cDNA: FU21541 fis, ct AX025194
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6 protein-coupled receptor 20	#37150TV ISCOUNT INCOME.	96.1
plectatin 2 (mouse) homolog	25700-WH	86.1
solute carrier family 10 (sodium/bile acid cotransporter family), member 1	NA OCOCA	86
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To the Company of the	NM_012098	1.98
transcription factor of If and experies HMC. best	NH_004703	1.98
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actin related protein 2/3 complex, subunit 18 (41 kD)	AA464753	1.97
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mucis and catherin-like	717	1.93
zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	M58297	1.93
eldehyde axidize 1	AB046692	1.93
cholesteral 2-hydrax/tae	NM_003956	1.93
angiotensin receptor 1	NH_004835	1.93
phodocin	H33478	1.93
retinoid A mesptor, alpha	NH_002957	1.93
guarine nucleotide binding protein (6 protein), alpha 11 (6q class)	AI040021	1.93
ertagrin, alpha M (complement component receptor 3, alpha; also known as (011b (p170), macrophage antigen alpha pohypeptide)	NH_000632	1.93
heat shock 70kD protein 1A	NH_005345	1.93
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hypothetical protein MGC11138	80004504	1.92
WW domain binding protein 4 (formin binding protein 21)	7	1,92
Conservate includes gb-AVQ21983.1 /DEF=Homo septiens cDNA FU11921 fs., clone HEH881000318. /FEA=mANA /DB_XREF=gi:10433322 /VG=Hs.306616 Homo septiens cDNA FU11921 f AKQ21983		1.92
Consensus includes gb/kL121981 /DEF=Human DNA sequence from clone RPS-1061(18 on chromosome Ip36.22-36.33. Contains ESTs, STSs, GSs and a Ep6 island. Contains the 5 part		1.92
dopartine receptor 03		1.92
CD6 antigen	NM_006725	1.92
X03453 bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	X03453	1.92
NT-AEN-S6 artigen	NM_016122	1.92
dhibinasa Jalka 1 (carblage dhycoprotein-39)	M80927	1.92
ghrine receptor, alpha 3		1.92
Consensas includes gb.NX021495.1 / DEF=Homo supiens cDNA FU11433 fb., done HEMBA1001121. / FEA=mBNA /DB. XREF=q:10432690 /UG=Hs. 287415 Homo supiens cDNA FU11433 fb. XX021495		1.92
Consensus includes ap ANO24602.1 / DEF = Homo statiens CDNA: FU20949 fts. clone ADSE01902, FEA=mRNA, DB, XREF=a:10436915 / JG=H3.220255 Homo statiens CDNA: FU20949 fts. 1 ANO24602		1.92
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endridorate (S-lipzorgenase	\$	163
cytochrone P450, subfamily IIIA (nightedpine axidase), polypeptide 4		5
hypothetical protein FU10430		5
Consumation includes gb.2861070.1 ABF = Human mRNA for T cell receptor, clone 16RA15. FEA=mRNA /FR00=1 cell receptor, AB8, XREF=gi:33508 /UG=Hs, 121492 Human mRNA for T cell res X61070		<u>.</u>
tripartite modit-containing 10	~	<u>e</u> .
variable charge, Y chromosome	NM_004679 1.	.9
cytodrome P4So, subfamily XI8 (steroid 11-beta-hydroxylase), polypeptide 2	X54741 1.	6 .
protein phosphatase 2, regulatory subunit 8 (856), alpha isoform	A803525 1.	16.

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consensus includes gb:N18917 (DEF = Human glucocerebrosidase gene 10-2, 5 end /FEA=CDS_1 //08_XREF=gj:183025 //UG=Ns.287396 Human glucocerebrosidase gene 10-2, 5 end	
QAAA451 gana product	
maulin-like growth factor binding protein 5	W65062
io3 transcription factor	AU145005
pervis, elpha	NM_018222
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1792 AGE	hypotherical protein FU11871	71120_MN	1.83
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## 1955/25 ## 19	Consensus includes gb.A0023798.1 /DEF = Homo supiens cDNA FU13736 fs. clone PLACE3000156. /FEA=mBNA /DB_XREF=gi:10435842 /UG=Hs.31532 Homo supiens mRNA; cDI	A DKFZp AK023798	1.83
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and) receipt (www.openoem process catalyck subunitation process	A478592	2.
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MAY OS 19	offactory receptor, family 7, subfamily A member 17	AC005255	1.82
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studenting receive higher & f. flurman paperloma virus t6-associated protein, Angelman syndrome	US4404 RC260658	
Constitution and protein	NM 001526	7.
refrontation (respons t	NH 015848	7
Procedural protein F122501	NM_024822	1.74
dromasome 4 open naking itame 5	NM_016599	1.74
emerin AS	NH_001154	7.7
growth differentiation factor 2	NM_016204	7.
hypothetical protein FU13448	NM_025147	7
forthwed but 0.2	NM_004474	<u>.</u>
System's Elisabeth (Colube)	NM 025076	
ripourous present lette. Indianalise commit forter bindian protein avid labile subsmit	AW338791	7.
Informer 14	NM_022046	7.
Consensus includes qb.AI275371 (DEF = Homo supiers partial 16/H13 gene for immunoglobulin heavy chain V region, case 1, clone 16 (FEA=105 (DB_XREF=9;7573002 /UG=Hs.277336 Ho AI275371	o A/275371	1.74
Consensus includes gic UB2306.1 DEF=Home sepiens unknown protein mRNA, purial cds. /FEA=mRNA /PROD=unknown /DB_XREF=gi:1938333 /UG=Hs.12308 Home sepiens unknown protein mRNA, purial cds. /FEA=mRNA /PROD=unknown /DB_XREF=gi:1938333 /UG=Hs.12308 Home sepiens unknown protein mRNA.	r 1182306	1.74
poliovinus receptor-related 2 (herpez-irus entry mediator 8)	NM_002856	£.7
L3424 & subdits dags, jajf, jaj6 genes corresponding to nucleotides 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	138424	2
four are a laid UN demants	AF220153	2 :
TABLE I SERVICE MEMORY IN PIRIL CASS I PROGOD	10000 HN	? ?
Office production	NN 030893	2 2
CONTEMPORAL OF STATE OF THE STA	AA443771	2
dexx, large (Ovescphik) homolog §	AB011155	1.73
Consensus includes gold: (2005:092.1 / DEF = Homo supiens, clone IMAGE: 3843012, mRNA, purital cds. /FEL=mRNA /PR00=Unknown (protein for IMAGE: 3843012) / OB _XREF=gi: 13477248 /A 8C005:092	1 BC005092	1,73
\$\text{gbs/N16715.1} ABF=Home supiers PR02829 mRNA, complete cds. FEA=mRNA /PR0D=PR02829 //DB JR8F=9;7959928 //UE=Hs,256256 Home supiers PR02829 mRNA, complete cds / A7116715	/ 1/16715	1.73
Company, type I, alpha I	MM_000088	2 :
gody arteaingen, godyn sutrataniy b, macrogodyn (with transmemorane signa).	N33473 RC440021	3 5
Process process or miscons	NM 014133	2
dermein	NH 020157	2
leukocyte inmunoglobulin-tilu meeptor, suthtamity 8 (with TM and ITIM domains), member 3	AF009644	1.73
capase 5, apoptosis-related cysteine protesse	NH_004347	1.73
Importantial protein FU20761	NM_017954	E :
DAY COSE Protein	NM_014148	3 5
possasum merary recursing dansing, intermed ?	46086736	3 2
incurrent me vol. respectively transfer and propriete a selfer carrier family 30 (first transacties) member 4	NM 013309	2.2
UAZ, member ILX occopere family	AW301641	1.73
matri metaltoproteinase 16 (membrane-inserted)	NM_022564	1.73
carbonypeptidae, virelogenis ilia	NM_031311	1.73
zanc finger protein 141 (done pdf2.44)	NH_003441	<u>.</u>
CONTRACTOR SPACES IN CONTRACTOR AND THE CONTRACTOR AND THE CONTRACTOR IN CONTRACTOR AND THE CONTRACTOR AND T	AA573805	3 5
defind in bladder carrier chromosome responsable to the contraction of	NH 014618	2
lipose protein	80001698	1,73
(GA) Odd protein	NM_014928	E :
information for the 10.033.4	ALU96/12	2 2
common uniques regions of the common of the	NH 017422	3 5
DK727566/0123 protein	AL080220	1.73
RAMONES protein	A/122905	1,73
solute camer (amity 26, member 3	NM_000111	2.73
CONSTRUCTION INCLUDES TO THE SET OF S	AMOL7721	2 2
SX fee deferming region () -but § (carconneck choles), autosomal secretorial)	NH 000346	2.5
Rund-Kins 1 (E. coli)		1.73
Consensus includes gb:AL137292.1 /DEF=Homs supiens mRNA: CDNA DIVT.24341.016 (from clone DVT.2434.1016). /FEA=mRNA /DB_XREF=gi:6807752 /UG=Hs.274573 Homo supiens	AL137292	1.73
Carpensus includes go:100627.1 /0EF=human toni repeal mna (clins close pcd-kgni-8), and, FEA=mRNA /08_XREF=gi:337653 //0E-Hs.203776 Human toni repeal mna (clins close and clins close and clins (close close in Kona close is Kon	1 K00627	1.73
hypothetial profess (1915)	NM_025003	<u>e</u> :
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secreted frizzled-retained protein 5	NM_003015	2
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Epstein-Bar vins induced gene ? (Iymphocyte-specific G protein-coupled recentry)	20700	2
hypothetical protein FU11561	NN 034551	3 5
Proothetical protein FLI20637	Cotto Hit	3 5
hims mercrass factor alphasische of revision 6.		3
Consequence included and MKG1491 EST AND THE TOTAL OF VICE AND	KH_00/115	
MANAGE ALL MAN STORES WAS A STORES OF THE ST	AV691491	2
	NM_014870	2
mamosy (appa-1, 3-) gyycoprotein beta-1, 4-N-acrylglucosaminyltransferase, isoenzyme 8	NM_014275	2
phosphodesterase 44, CAMP-specific (phosphodesterase E1 dunce homolog, Drosophila)		1,73
solute carrier family 7 (cabonic amino acid transporter, y+ system), member 8	AL365343	1.72
Consensus includes gb. AL035295.1 (DEF = H. sepiens gene from PAC 106H8, similar to Dynamin. FEA=mRNA (PR00=hypothetical protein, (DB. XREF = cit + 200217 (MG = Hs. 56175 H. sapiens	AL035295	1.72
MUF1 protein	NM 006369	2
6 artigen 78		: 2
offactory receptor, family 12, subfamily 0, nember 2		2
hypothetical protein FLI23091		, F
potassim praediving channel suffamily I member 13		2 :
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ACCOUNTS AND THE SECOND OF THE		27.
Catching Carried Control of Catching Carried Control of Catching C		1.72
Proposed promise 1932	NM_024592	27.
ADP robosylation factor 6	NM_001663	27
hypothetical protein PR02007	NM_018613	27.
mascle-specific beta 1 integrin binding protein		27
splicing factor, erginine/serine-risch 6		1.72
Consensus includes gb.AV025388.1 /0FF=Homo supiens cDNA: FU21735 fis. clone (OLF3350, /FEA=mRNA /08_XREF=qi:10437892 /0/G=Hs, 306808 Homo supiens cDNA: FU21735 fis. ch.N025388		1.72
neuropaptide Y receptor Y2		2
amadiko repeat protein ALEX2	287	2
sphingasine - I-phosphate Iyase 1	. =	1 2
Consensus includes ob 6005002.1 (DEF Home supiers skin-specific protein (m33) m8NA partial ces. (FRA=m8NA ACR)=clin-concein (m8 1005-01-01-01-01-01-01-01-01-01-01-01-01-01-		; ;
uncharacterized hypothalanus protein HT011		4 5
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dylamer recetor, metabolitose 8	=	2 :
Consensus includes gb.XL133018.1 (DEF = Homo sapiens mRNA: CDNA DIGZp43460327) (from clone DIGZp43460327). (FEA=mRNA (DB XRFF=m:6454498 AIK=H+ 270527 Homo sarians	AL 133018	ς t
dromosome 11 open reading frame 8	NA OUISE	۲ £
hypothetical protein 4796117.1		, 5
Lacte receptor, type 2, member 8		4 £
Conservate includes 90-XL355512 / DEF = Human DNA sequence from clone RP II - 487F5 on chromosome 6 Contains the 3 part of the GRIK2 (dutamate recentor ionotropic, tainate 2) cense.		! 2
interfeukin 6 receptor		4 2
transforming growth factor, beta 2	•	! 2
2 udit		: æ
sphingonycin phosphodesterase I, acid tysosomal (acid sphingomyelinase)		. ~
estatich	7	. ~
Compensa motivates go.XII (636.1 / OEF = H, superers clathrin light chain a gene. / F.E.A.=mRNA / O.B., XREF = gi.704460 / VIG=Hs, 285688 H, supiens clathrin light chain a gene	7.1 9291636 1.7	1.72
New Property (Property)	AF029729 1.7	~
iona sapiens mRNX: CDNA DKE 2658640617 (from clone DKFZp586A0617). NEA=mRNA /DB_XREF=gi:5911895 /UG=Hs.306342 Hama sapiens	AL117447 1.7	~
as years make 15.3 (The cast);	AF241534 1.72	~
(author) is an incodurate to the contract of t	NM_006089	~

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carbohydrate (N-scetydjucosamine 6-0) sufformasterase 7	AL022165
sprecan 1 (chandratin suffate proteophycan 1, large aggregating proteoghycan, antigen identified by monoclonal antibody A0122)	NH_001135
SUMMILES profess	162872
unchanging authorized parties 2/52P	WW 020669
reputitis della antigen-interacting protein A	8E966372
nterferon, alpha 4	
CORNEL STATES AND STAT	
deliconessociated protein VT.1	20C200_PA
chromosome 16 open reading frame 5	66E10_MN
ringless-type MMTV integration site family, member 108	NM_003394
OAN 1096 protein	BG261071
program minorities !	66034080
institution of the property of the contract of	9E9Z10 RN
CLAN 107 protein	AB029030
rstragen receptor I	A073549
COMBONIAN INCLOSES ST. 1. (DEF = Homo sepiens prostate-specific membrane antigen PSM mRNA, exon 6 alternative splice variant, partial cds. (FEA=mRNA, PROD=prostate-specific AP254357	ts. /FEA=mRNA /PROD=prostate-specific AF254357
information reduction 1	B(002511
NEXT (Rest-Vertical Conference of the International Conference of the Conference of	
LONGONIONES DE LANGESTO (1764-63) (100_ART =91,534-06/) (100_ART =631,8120104.3) (1,1016 =1) ARE 11036/33 (10=113,8306.3 NUCLE) ART 11036/33 (10=113,8306.3 NUCLE) ARTHUR DESIGN 3	eceptor subtamily 1, group I, member 3 AAb_8440 NM_CO2282
Natroción 1 (cationic antimicrobial protein 37)	002100 WN
consensus includes go AL 109809 (DEF = Human DM sequence from clone RP 4-673020 on chromosome 20. Contains a PTPNS (protein tyrosine phosphalase, non-receiper type substrate) (AL 109809	sphalase, non-receptor type substrate) / AL109809
CONSONIALS INCOLOCIES GRANT 20842 / FEA=EST /OB_XREF=gi:10817994 /OB_XREF=est:AV720842 /CLONE=6LCCOHO5 /UG=Hs.282435 ESTs	AV720842
ankyrin 3, node of karvier (ankyrin G)	NH_001149
der cysteine) proteinase inhibition, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_000295
Officialm-disk	8C000055
our many included the second of the second o	2803948 AIG=Hs 306987 Home services 8002821
Dinamin (dimenin) 2	
glycine amidnotranskerase (L-erginine:glycine amidinotransferase)	NH_001482
gastric inhibitrary pohypeptide receptor	NM_000164
aptin receptor	
manners and whoses go. ALTS / 90.1 / OEF = Homo suprens mRNA CONA DIV Zp434F1011 (from clone OK/Zp434F1011). /FEA=mRNA / OB_XREF = 9:7018535 / NG=Hs. 274589 Homo suprens	
WALKER FOR THE PROPERTY AND THE PROPERTY	AF334812
and your such assistant section of the control of t	
guarantees (USF13), mand. Agress (Espaie 13, gogiosis-related systeme proteise (USF13), mand. (FEA=mand Jeth=USF13 /FAU)= Proteisid bander protein	ase 13/UB_AKEF≡g:45025/U/U6≃Hs. NM_U03/23
derterin, alpha 3 (nicen (150kb), halinin (165kb), his 600 (150kb), exilentin)	CCCOO MM
wythrocyte protein band 4. I - Like 4	NH 022140
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demotion (C.4 mati) receptor-like 2	AF015524
COMPARTAN INCLUDES GO-ALON 7879 FEA-EST FOB_XREF =gi-4728067 FOB_XREF =est-DKTZP586H1222_s1 FLONE=DKF2p586H1222 FOG=H3: 194251 ESTS, Weakly similar to ALU2_HUMAN	il ESTs, Weakly similar to ALU2_HUMAN AL047879
hardkat athetion pretein, alpha	076833
Need shock 7000 protein 18 beneath after a mark at 11005 s	MM_005346
reproducted process truly to the second seco	NM_018043
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cholinaryic receptor, nicotinis, alpha polypeptide 3	8(000513
midine 1 (Opitz/888 syndrome)	AF041209
consorted by MOQ4451.1 DEF =Homo sepiens (DNY FU21198 fis, clone (OLO0220, FEA=mRNA, DB_MEF=gi:10437259 /UG=Hs. 306707 Homo supiens (DNX FU21198 fis, ct AK024851	07 Homo sapiens cONA: FU21198 fis, ct AX024851
COTAGETIVE SECTION OF FEMORE SECTION SEQUENCES THE MINISTRATION OF CONTROL OF EUROHAGE 29222. /FEM=MRINA /OB_XIEF=gi:5689802 /UG=Hs.140833 Home septens mRNA AL109671	2 /UG=Hs.140833 Homo sapiens mRNA AL:109671
Proposite T1, stateful, slow	A011712
23542. Office memoral seperals in a proteint I A emiancer binding protein chimera mithy. complete cds. // E.K.=mithy // 1900=E.W.S. proteint I A emiancer binding protein chimera // 08, XIEE (1956).	nancer binding proteinchimera /DB_XREF U35622
approximate promise in the contract of the con	NM_U245/6
	190300

decaymbonudease II, hysosomal	AB004574	
impristical alamina-rich protein kinase C substrate	NM_002356	1,71
hypothebical protein FL21963	NM_024560	1.7
H2A histone family, member N	NM_003514	1.71
brain specific protein	NN 016140	1.71
spiking bactor 34, subumit 2, 66kD	8000434	1.71
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La provincia de la projection de la proj	NM_002066	1.7
mynstoyktied alanme-nch protein lansse (substrate	M68956	1.7
tumor protein p73	NM 005427	17.1
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Service Service States Come (Lassass Mario), Complete (cd. //F.CA=mario), FRUU=FRU0838 /UB_AREF=g:11493408 /UG=Hs. 306360 Home sapiens clone FLB3535 AF130051	piens clone FLB3535 AF130051	Z.
Contains includes 90-A.1361/9 /UEF attumen DNA sequence from clone RP3-32214 on chromosome 6. Contains the SQX4 gene for SRY (sex determining region Y)-box 4, a pseudogene a AL1361/79	ox 4, a pseudogene si AL136179	1.71
KIAA0557 protein	AB011129	1.7.1
tumor stroms and activated macrophage protein DLH: 1	NN 030776	
IQAA1000 protein	2000000	: :
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Comment includes the comment of the	AF114013	1.71
and the second section of the second section s	NM_005576	<u>-</u> -
Consensus includes 90:84 858194 FEA= \$17 08_XREF = 91:10372818 /08_XREF = est:7919405.x1 /CLONE=IMAGE:3306920 /UG=Hs.323053 Homo sapiens mRNA full length insert cDNA cle BESS8194	ength insert cDNA clc BE858194	1.70
Consensus includes gib.MU144277 /FEA=EST /OB_XREF=gi:1005798 //OB_XREF =est:MU144277 //LONE=HENBA1001415 //UE=HS.296525 Homo sapiens cDNA FU10062 fis. clone HENBA AU144277	362 fis. clone HEMBA AU144277	1.70
ATPase, Ca++ transporting, plasma membrane 1	195711	92
solute carier tanily { sodium-demendent increasis shouthats cottaneously manker ?	1000 I	2 .
I DANIEL I STATE THE STATE OF T	H40895	1.70
Comments where 137.359 (VCF - Frames) DNA Sequence from First 1-361/ On Chromosome 10. Contains E315, 3135 and 6335. Contains the gene for the nebulette protein (NEBL ALIS7398	ulette protein (NEBL. AL 157398	2.70
protein (peptidyt-proty) dis/trans stemense) NIMA-interacting 1-like	NM_006222	1,70
transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	NH 003221	1 70
Tanasari, S.	4402	
The Control of the Co	01672010	0/1
יינו יינו אינו אינו אינו אינו אינו אינו	NM_013249	1.70
MK-wax, expressed in neurons (Drosophila)	NM_002930	1.70
integrin, white CD (patries) synoprotein (ib of lib/lile complex, anigen (0418)	102963	1.70
mostial 1,4.5-biphosphate receptor, type 1	L38019	1.70
ectonectectide triphosphate diphosphohydralese 3	NM_001248	1.70
purinergic receptor PZX ligand-geted ion channel, 4	NM 002560	1.70
CCR4 carbon catabolite repression 4-like (5. cerevisiae)	NA 012118	1 70
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refress and encounties are an experience of the control of the con		97.
The state of the s	A-172066	1.70
Con in a month of the control of the	NM_024894	1.70
cambine 0-octanoyitransismuse	NM_021151	1.70
surfactant, pulmonary-essociated protein B	102761	1.70
protein kinze, cGMP-dependent, type II	NM 006259	92.1
UR protein	COTTO MA	2 5
IDAN 1654 protein	1806141	2 .
c-myc binding prostein	00000	2 5
Consensus includes gb.Al.161956.1 /DEF = Norms sapiens mRNA. cDNA DKF22/61A17121 (from close DKF22/61A17121) /FEA.E.m.BNA /DR. 18FE = ni.7129 RDR 11C = He. 10C 402 House 1 and 10C 402 Ho		2.5
potassium channel subfamily II, member 7	NW 005214	2 5
Sp4 transcription factor	CHECOL MA	2.5
6 problem - Counted no meters 1.6	311500_FM	2.7
transmitted to 170 histories account and families (MAD first)	NM_023914	2.7
defends to the control of the contro	NM_016833	2.7
LICENSE AND A CONTROL OF THE PROPERTY OF THE P	NM_001925	0.70
Thornware programs are accounted to	AF250321	1.70
Creat wasted proceeding	NM_022120	1.70
Imponencial protein 1 U.23093	NM_024643	1,70
spinocean state a	AF126749	1.70
Consensus includes go.AL57428.1 (DEF = Homo sapiens mRNA, CDNA DIXZQ761F152 (from clone DK72p761F152), FEA= mRNA, (DB_XREF=gi.7018458 / NG=Hs. 306479 Homo sapiens	É	1.70
Latheren 3. (prostate specific antigen)	NH_001648	1.70
Consensus includes gb:8F031829 /FEA=ES1 //08_XREF=g5:10739541 //08_XREF=est:601557983F1 //LONE=INAGE:3827709 //UG=H1.2631 desmoqlein 2 //FL=qb:NN_001943.1		1.70
hemoglobin, alpha 2	150399	0,1
catamin (catherin-associated protein), alpha pseudogene 1	737994	02.1
transient receptor potential channel 6	NN OASS	
hypothetical protein DIVZ2p761D1823	4K026106	2.5
		.

solute carrier family 3 (systims, dibasic and neutral amino acid transporters, activator of cystims, dibasic and neutral amino acid transport], member 1	NH_000341	1.70
SWAIT/MUM.1 associated repressor protein	ALS24033	1.70
Typothetical protein Net, 3020	NM_024048	0. i
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Conservus includes gb.A.117549.1 /DEF=Norm supiers mRN4, cDNA DKZD586H0123 (from close DKZD586H0123). /FEA=mRNA /DB. XREF=ai:5912083 /UC=Hs. 268496 Homp supiers AL117549	sapiens AL117549	1.70
FXTO domain-containing ion transport regulator 2	X86400	1.70
\$0.06166.1 /DEF=Human SH3 domain-containing protein SH3P17 mRN4, complete cds. /F.EA=mRN4 /PR0D=5H3 domain-containing protein SH3P17 /DB_XREF=gi:1438932 /U6=Hs.3071 U6:166	:Hs.3071U61166	1.70
malanoma antigen, family A 6	U10691	1.70
macrophage stimulating I receptor (c-met-related tyrosine kinase)	NM_002447	1.70
CONSECTION SINCH SECTION OF LARGE ST 100 AREF = 915631009 / OB AREF = 641 mg 33109.11 / ALONE = IMAGE: 236921 / AG = Hs. 122158 ESTs.	A/911273	1.70
ESF-that-domain, multiple 5	BF110421	1.70
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Erdeofytan I. serrefor ormule	VM 002727	69
growth factor independent	NH 005263	69 -
Compensate includes gb.AL033539 (DEF=Human DNA sequence from clone RP3-477H2) on chromosome 22a12.1-12.2 Contains parts of one or two novel cenes. ES1s. 515.8 and 655s AEA=AL033538	s /FEA= AL033538	169
calequestrin 2 (cardiac muscle)	NH 001232	691
Consensus includes ga.AL.137403.1 /DEF=Homo septens mRNA; CDNA DV5/24434L092 (from clone DV5/24434L092). FEA=mRNA /DB_XREF=gi:6807951 /UG=Hs.306457 Homo septens mR	xens mR AL137403	1.69
lumitor in the second s	NM_007035	1.69
putable peratisone microbody protein 175.1	NM_015887	1.69
timeters hamdlag (Drasophilis)	AK000721	1.69
APese, H+K+ exchanging, beta polypopride	NH_000705	1.69
Stogma syndrome antigen 5 (autoantigen LJ)	6262859	1.69
Answers includes gb-M.0800068, I / DEF = Homo sapiens mRNA: CDNA DIV Zb5641062 (from clone DX/Zb5641062). FEA=mRNA /DB_XREF=g1:5262475 / U/G=Hs.272534 Homo sapiens	Ě	1.69
Lanca excess	AW134976	69'
protein systems procedurates, receptor type, U protein systems (Elifott te	NM_002839	69.
Alf The Protein Co. 1.	AKBO1040	6. 5
met proto-oncopene (hepstochte growth factor recentor)	RER20509	6 8
senul Inducible cytoleine A2 (monocyte chemotactic protein 1)	\$69738	69.1
transcription elongation factor (SII) elongin A2	NM_016427	1.69
Consensus includes go.P.(0.1203.1 / DEF = Homo supiens homeobox protein Og 12 (00L 12) mRNU, purisis (ds. / F.E.)= mRNU / GEH= OG.1 2 / PROD=homeobox protein Og 12 (0B_ 2REF = gr.297 AF023203	=gi:297 AF023203	1.69
menancycount arrange for us	X93006	69'
restructurations represent the property of the	NM_022915	69:
GAN 335 protein are encourage and encourage by grant and a second and a second and a second and a second and a	NA_005465	69: 19:
interfudio 18 (interferon-camma-inducine (actor)	NA DOLEC	3
news grouth factor receptor (TMFRS 16) associated protein 1	NK 014380	69:1
K3 histone family, member 0	NM_003532	1.69
Onal (Msp40) homolog, subfamity 8, member 6	AL355379	1.69
hypothetical protein FU13831	NH_024729	1.69
CONSMISS INCLOSES 19.1 (DEF HOme suppers CDNV FUZ1966 Fis, clone HEPOSG44, /FDX=mRNA /DB_XREF=gi:10438192 /UG=Hs.287688 Home suppers CDNV: FUZ1966 Fis,	6 fis, cl AX025619	1.69
Constitutes 40-M.117659.1 (DEF = Home supiers mRNA; cDNA DIF7258610624 (from close DIF7258610624). FEA=mRNA (DB_JREF=gi:5912252 /UG=Hs. 306353 Home supiers in AL117659	piens n AL117659	1.69
Complete and Complete	NH_005256	<u>.</u>
information promise in the second promise in	NA_018058	6.
UTI-3Th protein	034622 AC003007	69.1
) !

ACCORDING 10	xistad overupressed protein WOZZIZO I OBF=News supters CDNA FUIZOSB fis, clone HEMBB1002092. /FEA=mRNA /OB_XREF=gi:10433445 /UG=Hs.296688 Homo supiers CDNA FUIZOSB ! Bity 4, group A membar 2
19519 / DB_JREF=extEST381752 / U6=Hs, 291222 ESTs morphogenetic protein 8467 (8467) mBM, partial cds. / FEL=mBM / GEN=8467 / PROO=bone morphogenetic protein 8467 (8467) mBM, partial cds. / FEL=mBM / GEN=8469 ESTs, Weaky similar to AUC_HUMAI IIII AUI Cleoplannic protein 8467 (8467) mBM, partial cds. / FEL=mBM / DB_MEE=9;10432666 / U6=Hs, 289094 Homo supiens cDNA FULLIA112 How beginns to AUC_HUMAI IIII AUI Cleoplannic cds. / FEL=mBM / DB_MEE=9;10432666 / U6=Hs, 289094 Homo supiens cDNA FULLIA112 How begins controlled and controlled denuin, close HCC, 2809 Homo supiens cDNA FULLIA112 How begins cds. / FEL=mBM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 284651 ESTs SSENT / DB_MEE=ext: MC67010 / UCNE=CKLAYCOM / U6=Hs, 277961 Human Chromosome 16 & MC close (17987) / UNAM / US / U6Hs / UNAM /	A/230410 A/090913 A/090913
19519 / DB_JREF=ettEST381752 / U6=Hb_291222 ESTs morphogenetic protein 8467 (8467) mBM. partial cds. / FEL=mBM / GEN=BHP7 / PROO=bone morphogenetic protein 8467 (8467) mBM. partial cds. / FEL=mBM / GEN=BHP7 / PROO=bone morphogenetic protein 8467 (8467) mBM. partial cds. / FEL=mBM / DB_MEE=p\$:10432666 / U6=Hs_289094 Homo supiens cDNA FULLIA1218 / LEDT ett 18. done HENBALIO00876. / FEL=mBM / DB_MEE=p\$:10432666 / U6=Hs_289094 Homo supiens cDNA FULLIA1218 / LEDT ett 18. done HENBALIO00876. / FEL=mBM / U6=Hs_289625 Homo supiens cDNA FULLIA1218 / LEDT ett 18. done HENBALIO00876. / FEL=mBM / U6=Hs_289625 Homo supiens mBM / CDM / UCEp\$=641.1000-012-62 (400-1122) / Cds=UNBHOWN / QB=MC50166 / Vg=4884381 / Ng=Hs_26295 / Homo supiens mBM / CDM / U6=Hs_289694 Homo supiens mBM / U6=Hs_289644 Homo supiens mBM	
morphogenetic protein BMPT (BMPT) mBMA partial cds. /FEH=mBMA /FEH=BMPT /PROD=bone morphogenetic protein BMPT (BMPT) mBMA partial cds. /FEH=mBMA /FEH=BMPT /PROD=bone morphogenetic protein BMPT (BMPT) mBMA partial cds. /FEH=mBMA /FEH=BMPT /PROD=bone morphogenetic protein BMPT (BMPT) mBMA partial cds. /FEH=mBMA /FEH=BMPT /FROD=bone morphogenetic protein BMPT /FEH=mBMA /FEH=mBMA /FEH=mBMA /FEH=BMPT /FEH=MBMA /FEH=BMPT /FEH=MBMA /FEH=MBMA /FEH=MBMA /FEH=BMPT /FEH=MBMA /FEH=BMPT /FEH=BMPT /FEH=MBMA /FEH=BMPT /FEH=BM	
morphogenetic protein 8MP7 (8MP1) mBNA, partial cds. /FEA=mRNA /GEN=5MP7 /PROD=bone morphogenetic protein 8MP7 (8MP1) mBNA, partial cds. /FEA=mRNA /GEN=5MP7 /PROD=bone morphogenetic protein 8MP7 (8MP1) mBNA partial cds. /FEA=mRNA /GEN=5MP7 /PROD=bone morphogenetic protein 8MP7 (8MP1) mBNA complex cds. /FEU /GENST (10412 fts, done HEMBA10000376. /FEA=mRNA /DE_2765612 /ME=62.505667 /ME=16.288994 Home supiens cds. /FEU /GENST (10412 fts, done HEMBA10000376. /FEA=mRNA /DE_2765656667 /ME=16.288994 Home supiens mBNA complex cds. /FEU /GENST (10622) mBNA /GENST (106222) mB	
morphogenetic protein BMP1 (BMP1) mMM, partial cds. <i>FEbs</i> =mRMA /GEN=SMP1 /PX00=bone morphogenetic protein BMP1 (BMP1) mMM, partial cds. <i>FEbs</i> =mRMA /GEN=SMP1 /PX00=bone morphogenetic protein BMP1 (BMP1) mMM, partial cds. <i>FEbs</i> =mRMA /DB_MEF=g;10.432666 /MC=Hs.289094 Homo supiens cDNA /EU11412 h. FED11412 h, close HEHBA1 0000376. <i>FEbs</i> =mRMA /DB_MEF=g;10.432666 /MC=Hs.289094 Homo supiens cDNA /EU11412 h. LESS (SES) (MC=Hs.289094 Homo supiens cDNA /EU11412 h. LESS (SES) (MC=Hs.289094 Homo supiens cDNA /EBS) (MC=Hs.289094 Homo supiens mRMA cDNA /EBS) (MC=Hs.289094 Homo supiens mRMA /EBS) (MC=Hs.289091 HOMO /MC=Hs.289091 HOMO /MC=Hs.28	
morphogenetic protein 8MP7 (BMP7) mRNA, partial cds. /FEA=mRNA /KEN=BMP7 (PR00=bone morphogenetic protein 8MP (processin 8MP protein 8MP7) mRNA to make the control opalamic tall 1 FU11112 fst, close #EMBA1000876. /FEA=mRNA /RB_XREF=gi-10432666 /MG=Hs. 285954 Homo appiens cDNA /LU11112 h. FLU11112 fst, close #EMBA1000876. /FEA=mRNA /RB_XREF=gi-10432666 /MG=Hs. 285959 Homo appiens cDNA /LU11112 h. FLU11112 fst, close #EMBA1000876. /FEA=mRNA /RB_XREF=gi-10432666 /MG=Hs. 285855 Homo appiens mRNA. complete cds. /FEJ S6210 /RB_XREF=est-hi-12403.1 /LUNE=MNACRO /MG=Hs. 285855 Homo appiens mRNA. complete cds. /FEJ S6210 /RB_XREF=est-hi-12403.1 /LUNE=MNACRO /MG=Hs. 285855 Homo appiens mRNA. complete cds. /FEJ S6210 /RB_XREF=est-hi-12403.1 /LUNE=MNACRO /MG=Hs. 285855 Homo appiens mRNA. complete cds. /FEJ S6210 /RB_XREF=est-hi-12403.1 /LUNE=MNACRO /MG=Hs. 285855 Homo appiens mRNA. complete cds. /FEJ=mRNA /RB_XREF=gi-1394419 /MG=Hs. 306292 Homo appiens mRNA. /RB_XREF=gi-1394419 /MG=Hs. 306292 Homo appiens mRNA. /RB_XREF=gi-1394419 /MG=Hs. 306292 Homo appiens mRNA. /RB_XREF=gi-139492 /MG=Hs. 201420 E51s. Moderately similar in AUI7_MINMA AUI SUBSANA. /RB_MG-MG-MG-MG-MG-MG-MG-MG-MG-MG-MG-MG-MG-M	Tony receptor, tarrity 1, suddamity A. member 1 NN-2014565
55111 (DB_JBEF=ett=152603.1) KLONE=INMGE2767612 /UG=Hs. 193408 ESTs, Weakly similar to ALUC_HUMAN IIII ALU C begatarist tall 1 i-fU11412 fst, clone WEM8A1000876. FEL=mRNA /DB_JREF=gi:10432666 /UG=Hs. 289094 form sapiens cDNA FU11412 i. FU11412 tall 1 i-fU11412 fst, clone WEM8A1000876. FEL=mRNA /DB_JREF=gi:10432666 /UG=Hs. 289094 form sapiens cDNA FU11412 i. FEGE 10 /DB_JREF=est:WEB7010 /CLONE=IRMGE23981548 /UG=Hs. 284651 ESTs 83873 /DB_JREF=est:WEB7010 /CLONE=IRMGE23981548 /UG=Hs. 284651 ESTs 83873 /DB_JREF=est:WEB7010 /CLONE=GKCAYCOA /UG=Hs. 284651 ESTs 122 (from clone D072p564F133) /FEA=mRNA /DB_JREF=gi:1040011 /UG=Hs. 306292 form sapiens min obypospiles 2 123 (from clone D072p56671122) /cd==UNNOWN /gp=ALD50166 /gj=4884381 /ug=Hs. 26295 /fen=2654 1320 /DB_JREF=est:RC2-810318-110100-012-402 /UG=Hs. 201420 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAN Competence cds. /FEA=mRNA /DB_JREF=gi:3417290 /UG=Hs. 177961 forman (bromosome 16 BAC clone CIT987) Competence till 1 2 provein: 1)	
\$5111 (708_3REF=esting2e03.17 KLONE=INAGE22567612 (70E=Hz.193408 ESTs, Weaky similar to ALUC_HUNAN IIII ALU Coplannt tall. 1 FLU11412 fst, done HEMBA10000976. FEA=mRNA (708_3REF=gi:10432666 /VG=Hz.289694 Homp supiens cDNA FLU11412 LEGION 200914 supiens control contr	
\$311 / 708_XEE=est_272403.at / KLONE=INARE275612 / Jú=Hh. 193408 ESTs, Weaky similar to ALUC_HUNAN IIII ALUC (Digital to ALUC_HUNAN III) ALUC (Septemble 18, 1811 / 108_XEE=est_272403.at / KLONE=INARE2361548 / Jú=Hh. 285625 Home appiens milly. Complete cds. / FE \$2210 / 708_XEE=est_2hi 2403.at / KLONE=INARE2381548 / Jú=Hh. 285625 Home appiens milly. Cohy Diff-AlaAutt 9 (from Cohe Diff-Est-28) (And Est_284613) / FEA=mRNA / Digital Set_2846381 / Jú=Hh. 285625 Home appiens milly. Cohy Diff-AlaAutt 9 (from Cohe Diff-Est-28) / Ads=UNKNOWN / Jú=Hh. 284381 / Jú=Hh. 306222 Home appiens milly. Cohe Diff-Est-28001122 / Ads=UNKNOWN / Jú=Hh. 201420 ESTs. Moderately similar to ALU7_HUNAN ALU SUBFAN 1920 / Digital Set_28401131 / Ads=Hh. 306222 Home appiens milly. Translocated to . 2 Drosophila): Translocated to . 2	Tony receptor, tamby 5, subfamily V member 1 NN_033
Descrite Law, i. Gone HENBALLO00876. FEAL-mANA /DB_JAREF-ag: 10432666 /UG=Hs, 289094 Homo supiens CDNA FULLET II. FULLET IN, clone HENBALLO00876. FEAL-mANA /DB_JAREF-ag: 10432666 /UG=Hs, 285625 Homo supiens mithk. complete cds. /FE SCO. /DB_JAREF-ac: high Lab. 2.1 /CLONE=INAGE.2881548 /UG=Hs, 285625 Homo supiens mithk. cDNA DNC2p434ALL19 (from Control of Contro	mans include go ANTRESSES (FACET TO B. XRE = gicker) TO B. XRE = g
ische receptor superfamity, member 10c, deccy without an intracellular domain, clone MCC12787, m8NA, complete cds. /FE 56210 //DB_AXEFE=estinj12403.st //LONE=INAGE2981548 //JG=Hs.285625 Homo supiers mRNA, cDNA DNF2p4344119 (inp 201) 38873 //DB_AXEFE=estinj12403.st //LONE=GKLAYCO4 //JG=Hs.284651 E515. 38873 //DB_AXEFE=estinj12403.st //LONE=GKLAYCO4 //JG=Hs.284651 E515. 38873 //DB_AXEFE=estinj12403.st //LONE=GKLAYCO4 //JG=Hs.201420 E515. 122 (from clone DNF2p58601122) //ds=UNXHORN //Jp=AL050166 //Jg=4884381 //Jg=Hs.26255 //fen=2654 1920 //DB_AXEFE=estinj124 /JG=Hs.AVDB_AXEFE=gj:3417290 //JG=Hs.177961 Human (hromosome 16 BAC clone (TT98) AC clone (TT9875X-A-38804 //FEA=mRNA //DB_AXEFE=gj:3417290 //JG=Hs.177961 Human (hromosome 16 BAC clone (TT98) Problem: 1) Second of the complete cds. // FEA=mRNA //DB_AXEFE=gj:3417290 //JG=Hs.177961 Human (hromosome 16 BAC clone (TT98)) Problem: 1)	vanimuspykovarvania rasposi, polygopista i ali, 1 Taran induse polykki (141, 105E rhomo sasiens CNA ELIT 1412 fs. chen HENBA1000876, FEB.=mRNA (DB. 1815 era: 10437666 Alic=He 78964 Homo vanimos (PNA ELIT 141 7 A KNOT) sa
letter receptor superfamity, member 10c, decay without an intracellular domain, clone HGC:12787, mBNA, complete cds. //E	M243704
Increeptor superfamily, member 10c, decoy without an intracellular domain, clone MGC:12787, mBNA, complete cds. // FE 52210 // DB_LXBEF=esthji2203.sr // CLONE=INAGE:2881548 / US=H1.285625 Homo sapiens mRNA; cDNA DKE2pd34A119 (from 540) 88873 // OB_LXBEF=est:AVG87010 // CLONE=GKZAYCO4 / US=H1.284651 ESTs. 88873 // OB_LXBEF=est:AVG87010 // CLONE=GKZAYCO4 / US=H1.284651 ESTs. 122 (from clone DVE2p564F133 (from clone DVE2p564F133). // FEA=mRNA / DB_LXBEF=gi:4500011 / US=H1.306292 Homo sapiens mf 1920 // DB_LXBEF=est:AC2.870318.110100-012.402 / US=H1.201420 ESTs. Moderately similar to ALU7_HUMAN ALU SUBFAM 1920 // DB_LXBEF=est:AC2.870318.110100-012.402 / US=H1.201420 ESTs. Moderately similar to ALU7_HUMAN ALU SUBFAM AC complete cds. // EA=mRNA // DB_LXBEF=gi:398492 // FI=gb:114458.1 AC clone (ITJ875K-A-38804 // EA=mRNA // DB_LXBEF=gi:3417290 / UG=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 / UG=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 / UG=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 / UG=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 / UG=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 / UG=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 // E=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 // E=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=mRNA // DB_LXBEF=gi:3417290 // E=H1.177961 Human (hnomosome 16 BAC clone (ITJ875K-DF) and account in the complete cds. // EA=H1.177961 // EA=H1.177961 // EA=H1.177961 // EA=H1.177961 // EA=H1.177961 // EA=H1.177961 //	
istor receptor superfamily, member 10c, decoy without an intracellular domain, clone MGC:12787, mRNA, complete cds. /FE 56210 /DB_XREF=est:h 12403.x1 /CLONE=IMAGE:2981548 /US=Ht.285625 Homo sapiens mRNA, cDNA DIGZp434A119 (mp. 20) 2120 /DB_XREF=est:h/687010 /CLONE=6XCAYCO4 /NG=Ht.284651 ESTs 2121 (from clone DIGZp564F133). /FEA=mRNA /DB_XREF=gi:4500011 /NG=Ht.306292 Homo sapiens mf. 2122 (from clone DIGZp566F133 (mp. clone DIGZp564F133). /FEA=mRNA /DB_XREF=gi:4500011 /NG=Ht.36295 /Am=2654 2122 (from clone DIGZp586D1122) /cda=UNXNOWH /gp=AL050166 /gi=4884381 /ug=Ht.26295 /Am=2654 21320 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.201420 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAN 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.201420 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAN 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21920 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21020 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21020 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 Human Chromosome 16 BAC clone (CT98) 21020 /DB_XREF=est:RC2-810318-110100-012-402 /UG=Ht.177961 /UD=Ht.177961 /UD=Ht.17	
562 to 708_XREF=est:NES73.1 / KLONE=INAGE:2981548 / NG=H1.295625 Hamp stapiens mRNK cDNA DNEZp434A119 (trop 90) 88873 708_XREF=est:NES7010 / KLONE=EKKAYCO4 / NG=H1.284651 EST5 12. (DNA DNEZp564f133 (from clone DNEZp564f133), /FEA=mRNA / D8_XREF=gi:4500011 / NG=H1.306232 Homo stapiens mf 1920 / DB_XREF=est:RC2-810318-110100-012-402 / NG=H1.201420 EST5, Moderately similar to ALU7_HUMAN ALU SUBFAN 1920 / DB_XREF=est:RC2-810318-110100-012-402 / NG=H1.201420 EST5, Moderately similar to ALU7_HUMAN ALU SUBFAN 1920 / DB_XREF=est:RC2-810318-110100-012-402 / NG=H1.201420 EST5, Moderately similar to ALU7_HUMAN ALU SUBFAN 1920 / DB_XREF=est:RC2-810318-110100-012-402 / NG=H1.201428.1 At clone (CIT9875K-A-388D4 / FEA=mRNA / DB_XREF=gj:3417290 / NG=H1.177961 Human Chromosome 16 BAC clone (CIT987) Potentic Lail, 2 providen-1)	0050431 (OFE = Nome superes, Similar to tumor necrosis factor receptor supertamity, member 10c, decoy without an intracellular domain, close MGC12787, mRNA, compete cds. FEB 1000509
98873 / OB_XREF = est: AVE87010 / CLONE = GKCAYCO4 / JG = Hs. 284651 ESTs \$8873 / OB_XREF = est: AVE87010 / CLONE = GKCAYCO4 / JG = Hs. 284651 ESTs • COMA DIVEQSG4F 133 (from clone DIVEQSG4F 133), / FEA = mRNA / OB_XREF = gi-4500011 / JG = Hs. 306292 Hamos supiens mf 122 (from clone DIVEQSS6D1122) / Acb = UNXWORN / gp = AL050166 / gj = +884381 / Jug = Hs. 26295 / Ann = 2654 1920 / OB_XREF = est: RC2-810318-110100-012-402 / JG = Hs. 201420 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAN 1920 / OB_XREF = est: RC2-810318-110100-012-402 / JG = Hs. 201420 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAN Spion, complete cds. / FEA = mRNA / OB_XREF = gj:398492 / FL = gb.2.1 (458.1 AC clone (CIT9875K-A-388D4 / FEA = mRNA / OB_XREF = gj:3417290 / JG = Hs. 177961 / Human Chromosome 16 BAC clone (CIT987 Ms = 1) plasmic tail, 2 provien-1)	man inches publicista Chief 10 ARE = g1745C10 /08 ARE = cth/12403.x1 /CLONE=1NACE:2981548 AIG=Ht. 205525 Homo sapiens mRNA; cDNA DKT2p43.44119 (from AWG635
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P00 8	POU domain, class 4, transcription factor 3	A#205153	4.
- cydin-	cyclin-depandent kinase inhibitor IC (p57, Kip2)	W95363	8 3
Consen	COTABITION INCOMES OF DATA 100250 FEA=EST 708_XREF=gi-1647823 708_XREF=est:2n41410.s1 /TLONE=INAGE:550003 /UE=Hs.90869 Home sapiens clones 24622 and 24622 mRNA sea AA100250	AA100250	99
lascin (lacin (Storngylocentrotus purpuratus) homolog 3 (actin-bunding protein, testicular)	NM_020369	99.1
a corporate in the corp	words C. (Same, neutronal)	NM_001975	99:
053-00	sisters inclining (University of State Sta	AF039196	99.
-today	hypothetical protein F L1 (633	NM_022112	28
KOAO36	(UA036 protein	MM_018162	99.
gestrin	gustrin-refeasing peptide	MC/2839	2 3
tumor n	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	KC002794	<u> </u>
(sag	U6 snRNN-esociated Sm-like pratein	N37057	8 4
J.	zinc fingur protein 256	NM_007167	38
Current	WHITE ALL THE PROPERTY OF THE	AF144240	99.
spermid	Speriodischermen II. Las erktransferase, aum engennenn regulator ot chronalin, sublamiy e, member 1 Speriodischermen II. Las erktransferase	86289800	99.
empless	wingless-type MATV integration site termity, member 28	M55580 AR045117	9 5
Spese protein	Octor	AA209239	8 9
Town I	Authorities prosted protein. [-51A]	AF069681	9
IQA404S	3	NM_018992	99.
10AAO66		AW592563	3 8
c) samp		AF 201291	9 9
in Appara	ione peruzidase 2	AM406605	8 3
S C S		AV726646	8 3
- Grane	rponent of Ra-reactive factor)	AV686235	99
mediodes	akoura nubarak, viduzkeri. Litye, alpha 10 subuni: akadebalaki surakema i	8E550599	99:1
heurone	in factor DAT	NM_004991	9.
Consensu	XXEF= gi:11050855 /08_XXEF=est; QV4-HT0894-290900-399-c04 /JJ6=Hs 146200 F5Ts	AL050152	9 5
utintion		57,9561 NN 018961	3 3
Consensu	14 sequence from clone 153614 on chromosome 6p21.3-22.2. Contains the 3 end of the 2NF184 gene for Kruppel-like zinc finger protein	AL031118	8 15
Sanc tange		NH_003408	99.
4	Notes and the second of the se	N344415	99.
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fereign / hypothecizel protein DICZ_p76(1ND9)21 capican hemolog (Drosophila)	A920979 8F435376	
ripodinacial protein DIV £p/18 (NV9) 2.1 capican homolog (Divocaphila)	8F435376	1.66
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	AV755522	1.66
CONTENTIAL STATES AND PROPERTY FOR THE TOTAL STATES AND AND THE TOTAL STATES AND	quence 86109746	99'1
Consensus includes go. J. 099910, 1 (DEF althonia supiens cone HQ0262. IF EA = mRNA /DB _XREF = gi.6690195 /UE=Hs. 236760 Homo supiens clone HQ0262	AF090910	.6
magni, ceta i incrementa metapro, beta porpopride, antigen (0.29 includes MDF2, MSK (2)	M34189	1.66
Securities to experimental and an accompany of the control of the	NM_000840	1.66
Con 1711 instance granular control	NM_024803	1.66
Vitalization description (Vitalization Vitalization Vital	A8051523	1.66
animate and the management of the state of t	AF063612	99.
defend in hereboords landering 2	A1335208	99.
condition registers.	A-264787	8.
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Numer protein OSA that	NM_005424	99.
amadoblastin, enamel matriz protein	/82500_MM	8 3
myshold fymphoid or mised-lineage leukema (frithoras homoloo, Drosophila): Itanslocated to 4	A 040504	8 5
zinc finger protein-tilte 1	ALU43636	90.
atomal homolog 1 (Drosophila)	NH 005172	8 3
glucolánase (hezolánase 4, maturity onset diabetes of the young 2)	M69051	3 3
fortheed box 01A (fruitchorry countries)	AW117498	99.
Suctional Law	NM_001041	99
small protine-4ch protein 1A	NM_005987	39
Considerates includes go.XF 113683.1 / DEF = Homo suprens clone FLB 3521. / FEA= mRNA / DB_XREF = gi-8855610 / UE=Hs. 306569 Homo suprens clone FLB 3521.	AF113683	1.66
whereas a grant product	NM_014807	99.1
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hrondheite in reining	AX022688	1.66
Productival covine (U11807	NM_024997	99
Raf 2 interacting protein 8	44450_MM	9 5
hypothetical protein FU12616	MA_034995	99.
transition protein 1 (during histone to protamine replacement)	NM 003284	3 3
hypothetical protein FU11952	AX022014	991
Connectively, Co	NM_020435	1.66
may assist and a modernon site tarmy, member 3	NM_030753	1.66
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similar to stayforansferase ? ((alpha-N-acelyfneuraminy) 2,3-betaquaectosyi-1,3]-N-acelyf coaminide alpha-2,6-stayforansferase) E	NM 030965	86.
hypothetical protein FU20619	NM 017904	5 5
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Commenta includes go. Nebs24-4 F. Falser 103 (1) 18 (2) 2.	AV699347	1.65
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lather cell immunos/obudin-like meeptor, two domains, long ortoolsame tail. 4	Ar09/493	1.65
Consensus includes gb:ALG50002.1 /DEF=Homo supiers mRNA; cDNA DIGTp5640222 (from clone DIGTp5640222); /FEb=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA; cDNA DIGTp5640222); /FED=mRNA /DB :XREF=ci;4884256 (JIG=HS 94795 Homo supiers mRNA /DB :XREF=ci	MI AI 050002	ē 5
Consense includes go. M. 405975 FEA = EST FOB _XREF = gi: 6925032 FOB _XREF = est UI-HF-BLO-ACN-4-OS-O-UI-I / KLONE = IMAGE:3060368 / MG=Hs. 247721 Homo supiens done mcg33-54 i M405935	3-54 i AW405975	9
Approximate to the control of the co	NM_017860	1.65
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Fe framework of the control for a restrict of the control for	NH_016378	1.65
IGMMS 22 protein	U56236	1.65
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Consensus includes gotAn126763 /FEA=EST /08_XREF =gi-1686263 /08_XREF =sstzn87b11.3.1 XLONE=IMAKE:565149 /U6=Hb.182296 ESTs, Weaky similar to ALU6 HUMAN ALU SUBSA ALU SCREEN	18FAI AA 126763	5 5
branchibon elengation factor A (SII)-like 1	NM 004780	<u> </u>
hypodimizual protein FLI20307	NH 017757	591
basson (preynaptic cylomatri protein)	NN_003458	1.65
the second of th	NM_016563	1.65
Company of the state of the sta	NM_001868	1.65
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regions—extracted protein increating protein 3 trioughts mail creatinging in 1845 6 interacting protein 3	AB028989	9 3
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dytameta dehydrogenise	NA 005271	5 5
Pirin	NM 003662	5 5
Monean family namber 10	AB014606	5
lectin, galactoside-binding, solutble, 4 (palectin 4)	NM 006149	9
hypothetical protein MG(10771	NM 024506	59:1
nyosin 18	8F432550	.65
secreted trizzled-related protein 4	NM_003014	1.65
speciel AT-rich sequence binding protein 1 (binds to nuclear matrix/scathold-associating DNA's)	NM_002971	1.65
emocin A6	NM_001155	1.65
potassium invarish-recitying channel, subtamity I, member 15	U73191	1.65
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Or stands	AW189015	5
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dromosome 5 open neutro frame 4	H93077	59
X8831 protein	NM_014035	S
SAY (sez determining region 1)-box 5	NM_006940	1.65
gamma-amindoutyric acid (GABA) B receptor, 1	AL031983	1.65
AND THE PROPERTY OF THE PROPER	NM_014000	1.65
Companius includes gb_M024995.1 (DEF = Homo sequens cDNA: FU21342 fis, clone COL02673. /FEA=mRNA /DB_XREF=gi:10437426 /UG=Hs.306739 Homo sequens cDNA: FU21342 fis,	ct AK024995	1.65
restin (leed-Steinberg cell-azpressed intermediate filament-associated protein)	NM_002956	1.65
21/07/1 usinot granufoldu	NM_017937	.65
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0/6/1952 protein	AF245505	1.65
testicular haploid expressed gone	NM_016585	1.65
cholmenist receptor, introducis, beta polypopolice 4	NM_000750	1.65
Toron Nivare procedurates, receptor to provide 2 per	NH_002847	59:
upin person of parts concern 3.5 Providencies consult factor to be about 2.5	NM_014428	9:
potassium voltace-cated charmer, social subtamin's nember 5	NA_00338	9 9
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hypothetical protein FU11545		1.65
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indicator of group family family from the state of group family family from the state of group family fa		S 5
myekoid/hymphoid or mised-innege leutemie (trithorax homolog, Drosophila); translocated to, 4		1.65
Conserved includes gut/P023203 1 / DEF = Homo septiens homeobas protein Og12 (OGL12) mANA, purial cds. /FEA=mRNA /GEN=OGL12 /PROD=homeobas protein Og12 /DB_XREF = gi.299 / AF023203		1.65
A STATEMENT (2	1.65
vorweren andere grant 1984, Frent 1984, Fr		
transments are phosphatas with tensin homology	NW 013315	6 5
LIP protein; likely ortholog of mouse CRTR-1	NH 014553	59
fibroblast granth tactor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniolacial dysostosis 1, Crouzon syndrome, Pleiffer syndrome, Lackson-Weiss syndrome	H80634	.65
SH3domain, 6.882-tha, endophlin 82	80005407	1.65
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type I protein phosphatase inhibitor	NM 025210	9 59
TMO3 protein tyroxine kinase		59

thymosin, beta, identified in neuroblastoms cells	266120 MN	
hypothetical protein PAIC2X1	065507	
south carrier family 15 (postsymmytholoride frameworks).	Z81,650	9
nove godane som sinsa to 11001 y year nybonetoka on to protest nom boat ning	NN 002110	1.65
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Tables, pers. 5	ALS67012	<u>-</u>
endothelial PAS domain protein 1	NM_001430	<u>~</u>
Phypothetical protein FU10675	NM_018176	<u>.</u>
KIAA0161 gene product	NM_014746	<u> </u>
B reulanoma antigen	NM_001187	<u>-</u>
KQA0918 protein	AW449813	<u>-</u> .
socke carier family 1 (high affinity aspartate/glutamate transporter), member 6	NM_005071	<u>-</u>
spodipopratein L. 2	NM_030882	7.
Consensus includes gb:196936 (DEF =Homo sepiens systic fibrosis transmembrane conductance regulator (EFTR) gene, esons 23, 24s, and 24 /FEA=mRNA /OB_XREF=gi:180293 /UG=Hs. 1968936	93 /JG=Hs. M96936	<u>-</u>
Consensus includes gb:MA493300 FEA=EST NB_XREF=gi:2223141 /NB_XREF=est:ng97e11.31 //LONE=HMA6E:942764 /NG=Hs.104258 Homo sapiens mRNA, eson 1, 2, 3, 4, clone:RES4 AA493300	. clone:RES4 AA493300	<u>-</u> .
neurobophic tyrosine kinese, receptor, type 3	576475	-
A binase (PRIA) anchor protein (gravin) 12	AB003476	- -
y-yes-1 Yamaguchi sarcoma viral oncogone homolog 1	NH_005433	2
HIA-b associated transcript 1	AZ82485	ت
Section 1.	AW418882	<u>.</u>
TAIL PROGRAMMENT AT A TOTAL TO THE PROGRAMMENT AT	NN 015478	4 4
and 1) mayor on on unon (1) protections to the control of the con	86511164	
En Class artistion orders &	AW044631	- :
amphidonate 12-ficonomenae, 128 type	NM 001139	1.6
hypothetical protein LOC57138	KM_020433	1.6
Net, Ash and phospholipase (binding protein	A266839	79.
Consensus includes gb.M351043 /FEA=EST /OB_XREF = gi-4088249 /OB_XREF = est-qt22a08.x1 /CLONE=IMAGE.1948310 /UG=Hs.279477 ESTs	A351043	<u>-</u>
putative A-linked retinopathy protein	22/855	<u> </u>
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advancedulin receptor	NM_007264	7
Consumus includes gis \$511231 /FEA=EST //DB_XREF=gi:11594529 //DB_XREF=estUI-H-BI4-aci-q-11-0-UI.a1 /CLONE=INAGE=30852244 //UE=H-288582 ESTs, Weakly similar to ubiquitous BF511231	to ubiquitor: BFS11231	2
caspase 1, apoptosis-related cysteine professe (interfeulin 1, bets, convertase)	AJ719655	<u>.</u>
serine (or cysteine) proteinuse inhibitor, clade & (ovalbumin), member 9	8C002538	<u>-</u>
NECLY Washe brithough professional (1), cerevisiae)	80001364	3 3
The second secon	NM_023629	
goponessa posen rusani. Commensa inches de 16447105 FEA-EST OB 1885 mill 5177243 MB 1885 mel 7544400 zi KTONE-HMARE 3644180 MEHA, 281706 codiin i	MM_U22U82	<u> </u>
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Preuronal PAS domain protein 2	07570	9
CSR1 protein	NM 016240	7
a disintagin and metalloproteinase domain 3a (syritestin 1)	X89655	3
beta-emykaid binding protein precursor	AA012917	<u>.</u>
6 protein-coupled meaptor 31	662500_MN	<u>.</u>
windspeaked sodium channed beta-3 subunit (scn3b gene)	AB032984	3.
Cyclest Control gradual and Control and Co	NM_016323	<u>.</u>
Implementary prices MC 400	275420_PN	2 3
splotte care family 21 (ordanic anion transporter), member 9	AF205073	2
zinc fingur protein 291	AX025663	7
desmoptabin (DPI, DPII)	8E546897	<u></u>
Consensus includes gb.U00956.1 (DEF = Human clone KDBS.1 (CAC)n (GTG)n repeat-containing mRNA. FEA=mRNA. //DB_XBEF=gi-405058. //UG=Hs. 104112 Human clone KDBS.1 (CAC)n (GTG U00956	(CAC)n(GTG U00956	2
hypothical gene (6018	AL049786	3.
A kinase (PRKA) enchor protein 10	NM_007202	7
connectivity and an arrangement of the second of the secon	AF038567	<u>.</u>
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deskad in Beer cancer 1	AF026219	: :
ACO for serine protease homologue	NH 017509	: =
dopamine ne aptor 01	156987	=
solde carrier family 12, (potassium/chloride transporter) member 5	AF208159	<u>-</u>
ICAAOOO protein	D42044	-
hypothetical protein FU12294	NM_025100	J.
dremotex homeogy 5 (AT) alpha homeogy Dreschild.	107515	3.
terrance into year 2001 of 1012 minut total or to 2000	E	- :
CREATING Transcription correles subusit >	8(1053079	= :
Capase recutinent domain family, member 9	NM 022352	
Consensus includes gb.M026419.1 / DEF = Homa supiens cDNA: FU22786 fs. clone KAIA2150. / FLB=mRNA / DB XREF = m: 10439304 / UG=Hs. 306848 Homa supiens cDNA: FU22786 fs. cls ARD76439	fs. ck AX026439	
hypothetical protein FU12691	NN 024572	9
hydronan symbase 1	NM_001523	9.
translucer of ERBE, 2	AB051450	1.6
parameter and phospholipse (NM_016341	1.6
mendens prominent respira (Johnson-Esphessed unase, keratinocyte grown lactor receptor, cranotacial dysostosis), (rouzon syndrome, Piette syndrome, NH (1959))	drome_NM_022971	9.
dromosom 1 ocen making frame IA	U43568 UM 006383	
Consensus includes ab.NC086790.1 (DEF = Homo saziens scontase precursor (ACOH) mRNA nuclear cene encoding mitochandrial crotisina of FER=mRNA AGEN=ACON /PRO) = 2.00 (ACON /PRO) = 2.00	10=aro AF086790	-
VPS10 domain receptor protein	AB028982	
CORSOTION INCLUDED DISABLES AS MELEN TOB TAKE 9:2589627 TOB TAKE SETLEGGGCOB 3.1 KLONE=11MGE:1127918 AUG=11.270495 ESTs, Weakly similar to ubiquitous TPR motif. Y i AAG53456	otif, Y i AA653456	Ξ
MM_00136 dass, lafe (prospinal) formood 4 MM_00136	NN_001365	-
ANTICONE STATE OF THE PROPERTY	E NS. CF AXOZ4995 M 20646	
dgOI protein		
Consensus includes got AL 110201.1 /DEF = Home supiens mRNA: cDNA DIXZp586F1622 (from clone DXZp586F1622). /FEA=mRNA /DB_XREF = gi-5817120 /U6=Hs.278435 Home supiens		9.
monthlose-associated protein TA	AW296788	- -
myonecka potent FU1286	NM_024620	- -
Averages with the state of the	ome 4p AI697803	-
of distriction and metallicine in the mental of projections.	568277 AM	-
IJAN 1996 protein	AW301305	
Consersus includes go-XIO26720.1 /DEF=Homo supiens cDNA: FU23067 fs. clone LNG04993. /FEA=mRNA./DB_XREF=gs:10439638 /NG=Hs. 117167 Homo supiens cDNA: FU23067 fs. clone LNG04993. /FEA=mRNA./DB_XREF=gs:10439638 /NG=Hs. 117167 Homo supiens cDNA: FU23067 fs. clone LNG04993. /FEA=mRNA./DB_XREF=gs:10439638 /NG=Hs. 117167 Homo supiens cDNA: FU23067 fs. clone LNG04993. /FEA=mRNA./DB_XREF=gs:10439638 /NG=Hs. 117167 Homo supiens cDNA: FU23067 fs. clone LNG04993. /FEA=mRNA./DB_XREF=gs:10439638 /NG=Hs. 117167 Homo supiens cDNA: FU23067 fs. clone LNG04993.	7 fs, cl AX026720	9.1
MRE11 minoits recombination 11 homolog A (5, cerevisine)	80005241	1.6
Consentus anchodes go. 28 (837 i 70EF = H. sapiens clathrin light chain b gene. /FEA=mRNA /OB_XREF=gi:963046 /NG=Hs /73919 clathrin, light polypeptide (Lcb)	X81637	1.6
gycophorn A (includes RN blood group)	000178	1.63
Association of the control of the co	NM_016210	
acceptance II	M/9/281	<u> </u>
Leaf QL/ymphona 3	C-7510 MM	
hypothetical protein DIF 2p.56400462	AL033377	-
acid phosphatos, prostate	NH 001099	9 5
bipartite motil-containing 28	BE967532	.63
signal sequence receptor, alpha (translocon-associated protein alpha)	NM_003144	1.63
hypothetizal protein FU10043	NM_017979	1.63
Commensus modulets go.M915947 /FEA=EST / //08_XREF =91:5635802 //08_XREF =ettwg96e01.11 / TLONE=INAGE:2379096 //u6=Hs.28212 ESTs	Al915947	1.63
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Consensus includes gb.XW970948 /FEA=EST //08_XREF==qi:8160793 //08_XREF==qi:87383031 //16=Hs.269403 ESTs	AW970948	3 5
ets variant gone 1	X87175	G 1
hypothetical protein FU21162	NH 024873	1.63
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SWIGNE related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	AW152160	= :
systaine-rich motor neuron 1	86546884	20.
homso box (H6 family) 1	Z#ABIO WY	
bone morphogenetic protein 2	AS83044	
hypotherical protein FU22686	A825877	.63
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Consensus includes git,4984051 /FEA=EST (08_XREF=gi:S811270 /08_XREF=est:wtS2h03.x1 /CLONE=HMAE::2511125 /UG=Hs.11861 thyroid hormone receptor-associated protein, 240 A384021	ciated protein, 240 AUS4051	-
hypothetical protein FUI 3480	NM_025120	-
nephronophthisis i (juvenile)	NM_000272	_
supports (S. Mandhain (mentitate)	NM 004933	-
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catherin, ESF UNisseven-plass 6-type receptor 1 (filamingo homolog, Drosophila)	NM_014246	2 :
rypothetical protein from BCIA2 region	NM_014887	_
adenosine monophosphate dearrinase (isotorm E)	AA919119	_
22F-ilia protein	NM_016521	_
collagen, type III, aipha I (Ehlers-Danios syndrome type IV, autosomal dominant)	AU144167	_
dystodrewn, etchs	NM_001392	_
metrin 3-like (klishen)	NM 006181	_
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solute carrier lamily 4, sodium bicarbonate cotransporter, member 7	MM_003615	_
Oustar Ind. (18318:(18318 Hamp supiens cDNA, 5 end /clone=GEH-560E03 /clone_end=5 /gb=(18318 /gi=1579920 /ug=Hs, 123469 /en=519	C18318	1.63
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hypothetical protein FU21628	NA_030613	3.
charaideremia-ikke (Rab excort protein ?)	NM_001821	_
hypothetical protein DIGZp434W074	AL096732	1.63
Conserves includes ab:U79295.1 /DEF = Human clone 23961 mRNA sequence. /F.EA = mRNA /OB XREF = ai:1710277 /UG = Hs. 90866 Human clone 23961 mRNA sequence	U79295	1.63
the variant name 6 (TE) exercement	AF041811	1.63
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an exchanging a minimal state of the state o	202300 MM	3 3
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Hitochondria Acyt-LoA Thoesterase	/8/147A	. 63
Compensus includes abs/AQ25564. DEF Homo sepiens CDNA: FUZ1911 fis, clone HEP03855. /FEA=mRNA /OB_XREF=9:10438116 /UG=Hs.306816 Homo sepiens CDNA: FUZ1911 hs, cl ANO25564	A: FUZ1911 hs, cl AX025564	_
hairy/enhance-of-spiri related with TRPM motif I	R61374	.63
Cansensus includes gb:AV718487 /FEA=EST /OB_XREF =g:10815639 /OB_XREF =est:AV718487 /CLONE=GLCFYHO9 /UG=Hs.282656 ESTs	AV718487	_
Consensus incidicis ob. 179304. 1 (10 F = Human clone 23909 mRNA, partial cis. / FEA=mRNA /PROD=unknown / 70 J. XREF = gi:1710291 / VG = Hs. 281043 Human clone 23909 mRNA, partial ci V79304	09 mRNA, partial o U79304	1.63
distal-less homeo bas 6	NM_005222	
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XX mirror XX	A063189	-
appropriate process RS9184_	BF110434	-
\$5.005220.1 /DEF Home sapiens, Similar to chaperonin containing TCP1, subunit 8 (theta), close MGC:12240, mRNA, complete cds. /FEA=mRNA /PR00=Similar to chaperonin containin BC005220	aperonin containin BC005220	- 62

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	A8014531	79.
A word Develop by the sector of	AF247180	3.
Consensus includes go JAL110190.1 /DEF = Homo supiens mRNA; cDNA DNC 2656412116 (from clone DNC 2656412116). FEA=mRNA /DB_XREF=gi:5817104 /UG=Hs. 306338 Homo supiens in AL110190	104 /JG=Hs.306338 Homo sapiens n AL 110190	3.
glutamate receptor, metabotropic 5	NM_000842	3
serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1	KM 004353	29
code autombien, colein subfamily a 4	UN 003078	9
eritation-include finance	6/0700 PM	<u> </u>
POLITICE CONTROL OF THE POLITI	6/0400 PM	2 :
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21 a values reductive control of the	NM_031275	3
sufformatenase family, cytosotis, 28, member 1	NM_004605	1.62
Consensus includes go: H49382, FEA=EST /OB_XREF=g:1999223 /OB_XREF=est: yq:9bo6.31 /CLONE=INAGE:274115 /UG=H1.124984 ESTs, Moderately similar to ALUZ_HUMAN ALU SUSF# H49382	y similar to ALU7_HUMAN ALU SUBFA H49382	29.
Consumus includes gb:8F224076 /FEA=EST /08_XREF=gi+111113133 //08_XREF=est:7q83=q3.x1 /KLOHE=IMAGE:3704942 //UG=Hs.307438 Human DNA sequence from clone 495010 on c 8F224q76	UA sequence from clone 495010 on c BF224076	59.1
SH3-domain binding protein 2	48000462	3
alcohol dehydrocense (B (class I) hets onbyseride	COSTUM	<u> </u>
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synchronia (* 434), successing the (premodarbita-inducible), polypeptide /	NM_000764	3.
Zinc Brigar protein 144 (Mel: 18)	BC004858	29.
wingless-type MMTV integration site family, member 78	8E736994	39.
maprin A beta		3
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Company Laboratory Company Com	043/84	79.
Caronin (Caronin-Especiated protein), alpha i (1020)	NM_001903	3
neodern 1	AAS07012	3.
soluts carner family 22 (organic anion transporter), member 7	AF210455	79.1
N artino acid transporter 3	810810 MM	1.62
Consensus includes gb./XIO22397.1 / DEF = Homo sapiens cOVA FU12335 fs. clone MAMMA1002219, highly similar to Rattus nonvecicus reso70 mRNA. FEA=mRNA / DB XREF = ai. 1043328 XXIO22397	FEA= mRNA /DB XREF = ai:1043378 AX022397	2
myosin XVA	PEC310 MN	3
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interesting of president	13061	1.62
WM 4/3 protein	A8040906	<u>.</u>
LM protein (similar to ral protein linuse (-binding enigna)	8F671400	3.
CONTINUES INCLUDES DIA 070 266. 10EF = Homo sapiens clones 24611 and 24705 MRINA sequence. IF EA = MRINA 10B _ XREF = gi:3387934 /UG = Hs. 302042 Homo sapiens clones 24611 and	12 Homo sapiens clones 24611 and AF070566	29.1
hypotherical privian MGC10946	NM_030572	3.
HOOME TO COLUMN	8C001283	29.
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transforming, acidic collect-coil containing protein 2	-	2 4 1
innunoglobulin kupa constant		24
selectin L (tymphocyte adhesion molecule 1)		29.
chromosome 21 open reuking frame 2	828	3:
Consensus includes giz:(194644 /FEL=EST /08_XREF=gi:970039 /08_XREF=est:yq42a12.r1 /CLONE=HIMAE:198430 /UG=Hs.306542 Homo sapiens versitan Vnti isoform, mRNA, partial c& R34644		2 9 :
hypothetical protein FU22792	_	
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retrockstoms binding protein 9		<u>ت</u> :
jerty honolog-like (mouse)		<u>.</u>
ELAV (entryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen 0)	'n	2
hypothetical protein	_	<u>.</u>
phosphoinositide-3-kinase, catalytic, delta polypeptide	_	.
mandrane-spanning 4-domains, subfamily A member 2 (Fc fragment of Igf. high affinity I. receptor for, beta polypeptide)	010583 1.6	19
samme (or cystaine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member S		19.1
2.19 gunn		1.61
H4 histore family, member H	<u>~</u>	5
hypothetical gene FU00060	·	5
potasium inready-rectifying channel, subfamily I, member 3		<u>.</u>
replication protein A complex 34 kd subunit homolog Road		<u> </u>
plated extrating response homolog	308	; ;
Contractor (PASSO) / DEF = N suprens DNA for cyp related pseudogene. If EASTMINA / DB_AILD = 9:94 500 5 / Db_E Hs abents DNA for cyp related pseudogene.	9.1	
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Consensus includes gb.X90579.1 /DEF = H. sapiens DNA for op related pseudogene. /FEA=mRNA /DB_XREF=gi:945005 /UE=Hs. 166079 H. sapiens DNA for opp related pseudogene	X90579	19.
CONSTANT INCLUDES DE 169855 FEMBLEST 708, XXEF = 9:12603161 708, XXEF = est:60227952161 KLONE=INAGE:4367308 VIG=HS.49476 Homo sapiens clone TUA8 (n.du-chai region	. 86109855	5 3
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the control of the co		
The protein		5
hypothetical protein FU10619		19
hypothetical protein FU20813		5
gh:UB729.1 /DEF = Homo sepiens death addptor molecule RADD-2 mRNA, complete cds. /FEA=(DS //RAD=dath adaptor molecule RADD-2 //DB_XREF=gi:SOS1867 //FL=gb:UB7229.1	U87229	5
Consumes includes go.AL359557.1 / DEF = Homo sepiens mRNUx cDNA DNZ 274201415 (from clone DNZ 276201415). /FEA=mRNU /DB_XREF=gi:8655612 / UG=H3.306508 Homo sepiens	AL359557	5
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Total State of the	MH_003264 1.61	<u>.</u>
garne-armoonlyst acq (w.d.s.) A receptor, apra 5	AM_000810 1.6	. .
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dystruphin (muscular dystruphy, Duchenne and Becker types), includes 0X5142, 0X5164, 0X5206, 0X5230, 0X5239, 0X5269, 0X5269, 0X5272		- -
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call growth regulatory with Ef-hand domain	NH_006569 1.6	5

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	1.61
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: F=N:sapens gene tor I cell receptor gamma V region 5 /FEA=CDS_2 /DB_XREF=9:37009 /U6=Hs.247801 H.sapiens gene for T cell receptor gamma V r	69383 1.61
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ily, member 2	NM_004974 1.61
phosphotophnosini	_
	NN 002965
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Consensus includes go.16'052140. 70EF = Homo sepiens clone 23758 mRNA sequence. /FEA=mRNA /DB_XREF = gi.3350449 /NE=Hs. 141055 llono supiens clone 23758 mRNA sequence. NE	AF052140 1,61
IN uobrando	35
	NM_006543 1.61
	NM_001776 1.61
8_XREF=9 7318573 /08_XREF=es1.hh71e04.11 /CLONE=IMAGE;2968254 /UG=Hs.278541 ESTs, Moderalely similar to TYPH_HUMAN THYP	AW613387 1.61
I, grup I, member 3	NM_005122 1.61
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ranching enzyme, Andersen disease, ghycogen storage disease type IV)	
	N379338 1.61
	WF119875 1.61
PTEN induced putative kinase 1	
uncharacterized bone marrow protein \$H029	
	NM_020367 1.61
transport regulator 2	089
o sapiens done 23950 mRNA sequence. FEA=mRNA ADB XRFF=a; 3360396 AUG=Hs. 106620 Home saniens clone 23950 mRNA sequence	
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Consensus includes gb./L080232.1 /0EF=Homo sepiens mRNX: cDNA DIG 26/86A061 (from clone DIG 26/86A061). FEA=mRNA /0B: XREF==0; 5262725 /JIC=Hs. 220696 Homo sapiens mR AI 080232	
paired innunogobulin-ikia receptor alpha	•
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and PDZ) and no PDZ protein	53
	NM_005543 1,61
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166046.1 (DEF = Homo statiens clone 161455 breast expressed mRNA from chromosome 2. FER.= mRNA MR 1865 = mi-1619271 AIG=H4 02683 Home series slower	NH_U14699 1.60
	353
hypothetical protein FU20313 NM	• ~
es gb.4136548.1 /DEF=Homa sapiens mRNA; cDNA DK72p761618121 (from clone DK72p761618121); complete cds. FEA=mRNA /GEN=DK72p761618121 /PR0D=hypx.	36548 1.60
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111446	G=Hs.302046 Homo sapiens må sequence from clone 153614 or 18_XREF=gi:12654748, /UG=Hs. protein FU10624 IS Human mRNA for unknown pr
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61575501	G=H1.302046 Homo sapiens mB sequence from clone 153614 or 18_KEF = gi:12654748, /UG=H5. G sapiens cDNV: FUZ1490 fs, G protein FU10624
40, 1500 to the content point A	SEH13.302046 Homo sapiens må sequence from clone 1536.14 or 18_XBEF=gi:12654748, ME=Hb. protein FU10624 IS Human mRNA for unknown pr
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COOLOLY 10 RE skore sajent, Smile to RUMO029 protein, close HCC/50, mRNA, complete cds. FEU-mRNA, FROD=smile to RUMO029 protein, nB, RM (2007) Has 2, Mayer (Choosephal) Has 2, Mayer	18_XREF=9::12654748 /JG=Hs. 5 sapiens CDNA: FUZ 1490 fis, cb. protein FU10624 15 Human mRNA for unknown pn
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### 24 Page 1992	o sapiens CDNA. FUZ 1490 fis, d. protein FU10624 S Human mRNA for unknown pr
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hypothetical protein FU12345	65.1	
von Hippal-Lindau syndrome	NA_U2498/ 1.59	
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Consensus includes gb:R71245 /FEA=EST / OB_XREF=gi:844762 / OB_XREF=est:yi54e05.s1 / CLONE=INAGE:143072 / UG=Hs. 174303 ESTs	R71245	.59
1.ddby homdiag (mouse)	U82467	1.59
hypothetical protein FU11800	NH_024974	1.59
I institute in	H19843	.59
B-cell CLL/ymphoma 7A	80002629	1.59
cacherin 20, type 2	AF217289	1.59
Consensus includes gb:XW022038.1 / DEF = Homo supiens cDNA FU11976 fis, clone HEH881001253. / FEA=mRNA / DB_XREF = gi:10433356 /UG=Hs.296679 Homo supiens cDNA FU11976 i A0022038	f AK022038	1.59
IQA0944 protein	AB023161	1.59
FIX517	AF315951	1.59
growth factor receptor-bound protein 10	90990	1.59
Consensus includes ab./MO24185.1 /DEF=Horno sapiens cDNA FU14123 1s, clone HAMMA1002155. /FEA=mRNA /DB./XREF=qp:10436502 /UG=Hs.269314 Horno sapiens cDNA FU14123 14/8024185	1 AX024185	1.59
Compensus includes ab ALOSO1451 (DEF = Home samens mRNA: CDNA DICT. 25.586.C2020 (from clone DICT. 25.586.C2020) (FELS = mRNA, OB XREF = m; 48.84356, /UG = Hs. 2.25.986 (Home samens ALOSO145)	AL050145	1.59
shot status benedes: 2	AI816713	1.59
1000 T	AW663712	1.59
transmentione protein with EGF-like and two follistatin-like domains	85439316	1.59
··· interferon, alpha-inducible protein 27	NM_005532	1.59
10000042 protein	AW117368	1.59
horms but [1]	NM_021192	1.59
the curvine archarce (AEE) 12	KM_015313	1.59
Consensus includes to AULY 50943 FEA EST 708 XREF = a: 11012464 //08 XREF = a: AULY 50943 / (LONE = NT ZRP 2003984 / NG=Hs, 66762 Home supiens mRNA; cDNA DIGZp, 564A026 (from AUL) 50943	n AU150943	1.59
of a ferillary acids protein	NM_002055	1.59
ATTea. (4++ transporting, plasma membrane 3	AW615612	1.59
hypothetical protein FU22282	NM_024792	1.59
homo bus 66	A527340	1.59
WONtubiquinane axidomeductuse MLRQ subunit homolog	NM_020142	1.59
siabythanstense 44 (beta-galactosidase alpha-2,3-sia)transfense)	NM_003033	1.59
dymotypainogen 81	NH_001906	1.59
asyt-Coenzyme A dehydrogenase, C-2 to C-3 short chain	NM_000017	.59
ficolin (collegen/fibrinogen domain-containing lectin) 2 (hucolin)	NM_015839	.59
includents, alpha-	MA_002239	6 9
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hat domina de ID 3	NH 014606	1.59
MATERIA 2	AA608820	5.5
phosphorytae laisse, garma (/muscle)	NM_006213	1.59
cardigae intermediate layer protein, nucleotide pyrophosphotydrotase	NM_003613	53
BM1-associated protein 2	BC002495	1,59
Consensus includes gis/4.139318 /DEF=Human DNA sequence from clone RP11-124817 on chromosome 13. Contains the DCT gene for obsachrome lautomerase (dopachrome delta-isomer: AL139318	. AL 139318	1.59
Consensus includes gb: ALO49767 /DEF = Human DNA sequence from clone 172H20 on chromosome 20q12-13.12 Contains genes for semenogelin I and II and PI3 (protesse inhibitor 3, skin - ALO49767)	. AL049767	1.59
hypothetical protein FU21065	NM_022481	.59
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hypothetical protein DIG72p761F2014	NM. 020215	55
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phosphodistense 40, cAMP-specific (phosphodiestense E3 dunce homolog, Drosophilia)	AF012073	
lethal (3) malignant brain tumor I(3) mbt protein (Drosophila) homolog	KH 015478	5
95.M36841.1 /OEF=Muman serotomin receptor type 2 (SHT2) mRNA, complete cds. /FEA=mRNA /GEN=SHT2 /PR00=serotomin receptor // DR XREF=m:177775 /FI=mh-M86841.1	H86945	3 2
brin-derved neurotrophic factor	NA 001709	3 5
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protein phosphatase 3 (formerly 28), catalytic subunit, alpha isoform (calcineurin A alpha)	NH 000944	9 3
caterin (catherin-associated protein), beta 1 (88kD)	406100 MN	5
scrape responsive protein 1	NM 007281	3 5
dual specificity phosphatase 4	102 CO. MN	8.5
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hypothetical protein LOC57821	NW 021178	2 5
ectodemal dysplasia 1. anhidrotic	46061192	2 2
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Consensus includes gb.36'090886.1 /DEF=Homp supiens clone HQ0072, /FEA=mRMA /DB. XREF=q:6690183 /DG=Hs.284192 Homp supiens clone HQ0072	AF090886	8 5
putative anytrin-repeat containing protein	KW 015623	
paraconase 1	NH 000446	3
adenozine A1 receptor	X68485	3 5
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3-phosphoinositide dependent protein kinase- I	NM 002613	3 5
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transiert receptor potential channel 3	1147050	3 5
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hypothetical protein FU23506	NM 024833	3
exportin, IRMA (nuclear export receptor for IRMAs)	A/984005	85
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sytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	400.000
LASPS and FADD-like apoptosis regulator	
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hypothetical protein FU22419	1186003
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\text{\text{Now supplement 12 A-domains, sublamity A. member 7} \text{\text{\text{born animal MA. CDM. DAT. PSS-64.233}, FEA=mBMA .0BXBEF=gi:4500007 /UG=Hs. 302050 Home supplement mather animal MA. CDM. DAT. PSS-64.233 \text{
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MCF-binding transcription factor Dhangfei	AA521272	1.55
transmembrane, prostate androgen induced RNA	NM 020182	1.55
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hypothetical protein FU14033 similar to hypotia inducible factor 3, alpha subunit	AX021881	1.55
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regulator of 6-protein signaling 12	AF030111	1.55
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microtubule-associated protein 1A	AF095910	1.55
gap junction protein, beta 3, 31kD (connezin 31)	NH_024009	1.55
Down syndrome critical region gene 4	NM_005867	1.55
hypothetical protein PRO1995	NM_018612	1.55
ATP-binding execute, sub-family ((CFTR/MRP), member 6	A074459	1.55
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hypothetical protein FU10620	NA 018157	1.55
tumor metrosis factor receptor superfamity, member 10c, decoy without an intracellular domain	NH_003841	55.
FIJ murine oxteosarcoma viral oxcogene homolog B	NM_006732	1.55
dycine-N-cytransferase	EEC#CUMP	1.55
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hypothetical protein FU14033 similar to hypoxia inducible factor 3, alpha subunit	NM_022462	<u>.</u>
gerany/geranyl diphosphate symbase 1	AW299507	X.
double-stranded RNA specific adenosine dearmass	MM_018702	X :
IQAA IQZ3 protein	AL133033	X.
selectin E (endothelial adhesion molecule 1)	NH_000450	<u>.</u>
glutamate receptor, metabotropic?	NM_000844	X
similar to rat brearbarylate carrier-like protein	NM_030971	35.
CD3-epsidon-associated protein; artisense to ERCC-1	NM_012099	3.
UDP-фиказе фећуфтоденызе	NM_003359	<u>.</u>
zinc finger protein 37a (XOX 2.1)	AU118165	3.
postmeiotic segregation increased 2-like 3	038437	2.
Direc Anger protein 264	AF317549	5.
tests specific protein, Y-linked	M94893	3
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small potentials extension 8 surfaces (Nex. Live motif) member 13 (8-cell chemoattractum)	NH 006419	35
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thymine-DNA ghycosytase	BF674842	3.
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tissue factor pathway inhibitor (hipoprotein-associated coagulation inhibitor)	AF021834	Į.
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charide channel, calcium activetaed, family member 2	NM_006536	3
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adenylate binase S	NM_012093	<u>.</u>
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solute carrier family 8 (sodium/calcium exchanger), member 1	9	: 22
S-hydrax/byptamine (serotonin) receptor 4		
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metanoma antigen, family A. 4	AW438674	5
a dissintagins and metalloproteinase domain 12 (mettrin alpha)	NM 003474	2
rearin 3	NH 018399	25
glucagon-lite paptide 1 receptor	NH 002062	2
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barsforming greath factor, alpha	AF149096	2
Consensus includes 90:184942 /FEA=EST /08_XREF=gi:1196262 /08_XREF=est;w:38b08.s1 //LONE=IMAGE:244983 /UG=Hs.276590 ESTs	NS4942	1.53
homes bat (6	NM_004503	1.53
dead ringer (Drosophita)-like 2 (bright and dead ringer)	NM_006465	1.53
hypothetical protein FU11827	NM_025093	1.53
semelaryme repetitive matrix ?	AI655799	1.53
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hypothetical protein FLI20378	NW 017795	3 5
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Zem-specific argogeness inhibitor 3	NH_001704	1.53
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transcriptional activator of the c-tos promoter	NH 006365	3 5
hypothetical protein FU2025S	NM 017728	: 5
hypothetical protein FU10134	NM_018004	2
I FEA=EST (DB_XREF=gi:112634 /DB_XREF=estyz50h10.s1 /CLONE=IMAGE:265219 /UG=Hs.26968 Homo sapiens mRNA from chromosome 5q21-22,	clor N21364	1.53
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mannosyl (alpha-1,3.)-glycoprotein beta-1,4-Naceylglucosaminitrassierase, isoenzyme A	NK 012214	3 5
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instructions expected 1-like 1	NM_004739
Tytophan Z, 3-dextygenase	NM_005651
The state of the s	MM_00253/
onservations by the stage of th	m/ AL390149
broartte motif-containing 14	BC006333
zinc finger protein 74 (CoS2)	NM_003426
ONSWITCH IN THE SEST FELEST FOR THE FIRST FOR THE EXTREMENTAL SEST FOR THE MANNET 100 3031 1/16 = Hz. 287627 Homo sapiens CDNA FULL 151 fs, clone MANN AU148255	4H AU148255
Conservus includes gb.XX023345, TOEF E-Homo sapiens (ONA FL)13283 fis, clone OVXRC1001113, highly similar to Homo sapiens diaphanous 1 (HBIA1) mRNA. FEA=mRNA (OB_XREF=g AX023345	=g AK023345
Transactive attention propriet increases	NM_003382
Tues required to the second control of the s	MM 002750
Ontochome P450 subtantly III (mechentrain 4-hydravlase), polybeatide 18	NM 000772
erlangin, beta S	AL048423
RAMONS gave product	NM_014638
hypothetical protein EL122059	NM_022752
LOTATIONS GENERAL MANUAL STATE FOR SACRETS CHAN FULLS OF ITS, CIONE PLATINATION ISSS. (FEATHERING AND SACRETS) (1943/45 / 1944	11 1 AK022363
July 16 one product	NM 014705
melanoma unigen, family A. I (directs expression of antigen N.2.2.E)	NM 004988
putative Namo suppressor	80004483
COTSONIUS INCOLUGES DE STATO BLANDE STONE	AV763520
doms I homotog Z (L. delgama)	AF059252
Marky orbitog of mouse press lite homotogy [(Drosophila) like	MM_018068
manu mrangavienase (registropie caudemase) Consensis debas de Arisa visitos (ANY EL) 1494 fs. dous (OLISSA AFA MANA ANA ARISE AHA ANA ANA Anama anima (DAM EL) 1494 fs. dous (OLISSA ANA ANA ANA ANA ANA ANA ANA ANA ANA	MM_UUC424
photoin-lise series (1950)	AK022802
hypothetical protein FU11042	NM 018308
tor interacting serine-thrusonine linase 2	AF027706
Consensus includes gi:185910600 FEL=EST DB_XREF=gi:10407359 /DB_XREF=est:601501171F1 /CLONE=INAGE:3903161 /UG=Hs.288751 ESTS. Highly similar to HIC protein isoform p 185910600	p BE910600
vitamin D (1,25- dihydropyritamin D3) receptor	AA904259
Lapan 2, (1911) large substantial state of the control of the cont	H23254
ripponence promise to the same	NW DOOGS
Oyandarwin, alpha	U46745
hypathetical protein DIGIp/5100113	NM_018409
solute carrier taminy 21 (prostaglandin transporter), member 2	NM_005630
striated muscle contraction regulatory protein	M96843
Inchesporal EEO	T08613
Internet and Inter	AF234254
MAN 100 5 PATRON Innovikula America [11754	NM_018263
injection of production of the control of the contr	116464
Consensus includes apJAK025026.1 (DEF=Horns supers CIDA: FUZ1373 fis, clone COL03214, FEA=mBNA /NB. XREF=q:1043746; /UG=Hs, 306747 Horns supers CIDA: FUZ1373 fis. c. A0025026	d- AX025026
Consensus includes gb:263118 /OEF=H sapiens DNA for cestrogen receptor gene promoter /FEA=(DS /OB_XREF=gi:35159 /UE=Hs.247938 H:sapiens DNA for cestrogen receptor gene prv &63318	rt X63118
paired basic arrino acid cleaving ensyme (furin, mambrane associated receptor protein)	NM_002569
seamheithmenthe kinkas with DB- and plectatinh homology domains	NM_007064
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nematories process. DESTACEMENTS circular to investment into a constitute de constitut	A80145/4
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3 GAWQ23991 / OEF = Homo sasiens cDNA FUL 1847 fs. close THYR01000852 highly similar to Human branched-chain amino acid aminotransferase (FCA40) mRNA	76337B
kel adversion lunase pp 1.25	NM 015071
AA271. member IAS oncogene family	NM_004163
F=Homp sapiens cDNA: FU23475 fs, clone H3113659. /FEA=mRNA /DB_XREF=gi:10440177 /UG=Hs,288982 Homp sapiens cDNA: FU23475 fs,	ck AK027128
TOTOMISSION E 1 OF MAKENING THAN 80	NH_015227
Applications and construction of the construct	NM_018674
Proposition over an experiment of the control of th	ALU/3281
sprouty homolog 1, antagonist of FGE signaling (Drosophila)	
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CONSTRUCTOR SOOKS 1 (297.1 7027 # Home superis mKNX, CUNA DIV 4p54/7 34 (from clone DIV 4p54/7 34). / FEA=mRNA / DB_XREF = gi: 12224853 / UG=Hs. 47.867 Home superis in ALS 2687		
S-hydracytryplamine (serotonin) receptor 7 (ademylate cyclase-coupled)		
god phosphopriem 2	NM_016548 1.52	
mostra 1, 4, 3-traphosphate 3-trass (
hypothetical protein FU14249 similar to HS1 binding protein 3	Ş	
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vanilion receptor subtype I		
hypothetical protein FU12673		
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Persoriptional adaptor 3 (ADA3, yeast homolog) like (PCAF histone acetylase complex)	1	
biller cell lectin-like receptor subtamily (, member 4	1.52	
Barin containing monocarygenase 4		
retinois aid receptor, beta		
any hydrocarbon receptor	-	
fordiast growth tactor receptor 2 (bacteria-espressed kinase, keratinocyte growth factor receptor, cranisfacial dysostosis 1, Crouzon syndrome, Pleiffer syndrome, lackson-Weiss syndrome	A8030073	
endogin (Oster-Rendo-Weber syndrome 1)	BE732652 1.52	
sodute carier tamity 7. (cationis, amino acid transporter, y+ system) member 10		
Compensus includes gb:86231551 /FEA=EST /08_XREF=g:12726658 /08_XREF=estnal29h05.a1 /XLONE=IMA6E:4142457 /NG=Hs.74861 activated RNA polymenase II transcription colact 86231551	d 8G231551 1.52	
pkaninogen-iike		
PNO1992 protein	103	
Consumus includes gb:U92922.1 /DEF = Home supiens clone DT1P1A11 mRNA, CAG repeat region, /FBA=mRNA /DB, XREF=qi:2781410 /UG=H15, 168303 Home supiens clone DT1P1A11 mR1 U92992	1,52	
Mizzhed homolog 7 (Drosophilia)		
gb: AF 130053.1 / DEF = Homo suppiens clone FLB 4228 PRO1095 mRNA, complete cds. /FEA=mRNA, /PRO0=PR01095 //DB_XREF=gi: 1 493412 //JG=Hs. 302145 Homo supiens clone FLB 4228 AF 130053	8 AF130053 1.52	
Consensus includes gb:ALOSOO43 1 / DEF=Homo sepiens mRNA; CDNA DNFZp566H0524 (from clone DNFZp566H0524), /FEA=mRNA /DB_XREF=gi-484285 /UG=Hs.306310 Homo sepiens ALOSOO43		
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bline call immunogobokin-lise receptor, two domains, long cytoplasmic (ai), 4		
solute carrier family 4, sodium bicarbonate cotransporter, member 4	-	
nuclear receptor subfamily 2, group C, member 1	M21985 1.52	
distalge homolog 3 (Vanopus Inevis)	_	
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rypothecia protein 1111/13		
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maker, rice from retain 2	26.1 066/10_PM	
(DA0945 protein		
Consuments includes gb:8E551219 FEA=EST /DB_XREF=eig-9792911 /DB_XREF=est:7056011.x1 /CLONE=IHAGE:3222221 /UG=H1.(6762 Home studies) mRNx: (DHA DKZ256462062 (fm BESS)1219		
Consensus includes go AKOOO995.1 DEF = Homa sapiens cDNA FU10133 fs, clone HEHBA1003067. IFEA=mRNA /DB_XREF=gi:7021998 /UG=Hs.272209 Homa sapiens cDNA FU10133 fs, AKOOO9995		
(D1E artigen, e potypeptide		
protein phosphalase 1, regulatory (inhibitor) subunit 30		
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	ministration garman recipion 1	AF056979	3
	soure Land tamiy & (neurotansmiter transporter, gykine), member >	A-142501	3
	hypothetical protein HC(10902	NM_030570	25.
	hardest gram Letter 14	NA_004115	3
	podassum volage-gated channel, KQ1-like subfamily, member 3	NH_004519	1.52
	milt zii gobule-Ed Tartor 8 protein	8003610	2.5
	upha bulassema/mental retardation syndrome X-linked (RAUS4 homolog, S. cerensiae)	80002521	3.
	med transforming oncogene (derived from cell line NKI 4). RABS homolog	6(002977	1.52
	interbakin I, beta	NM_000576	3.
	dstabled homolog 2, mitogen-responsive phosphaptatein (Drasophila)	NH_001343	25.
	sycfin-dapendent binase-like 1 (CDC2-related binase)	NM_004196	1.51
	chromosome 9 open reading frame 7	NH_017586	1.51
	RAA1330 protein		1.51
	Consensus includes gb.14.137435.1 /DEF = Homo supiers mRNA; cDNA DKF2p76160924 (from clone DKF2p76160924). /FEA=mRNA /DB_XREF=gi:6807994 /UG=Hs.274577 Homo supiers	ms AL137435	1.51
	dopamine receptor 02		1.51
	Consensus includes gb.NF090887.1 /DEF=Homo sapiens clone HQ0085. /FEA=mRNA /DB_XREF=gi:6690154 /NG=Hs.306562 Homo sapiens clone HQ0085	AF090887	1.51
	S-hydrayotyptamine (serotomin) receptor 38	NM_006028	1.51
	ado-bato reductase famity 1, member 810 (adosse reductase)	NM_020299	1.51
	bromodomain and PKD finger containing, 1	NM_004634	1.51
	methylmalonate-semialdehyde ddrydrogenase	AF130089	1.51
	Consersus includes gb:AKQ25177. I DEF =Homo sepiens cDNA: FU21524 fis, clone COLO5921. FEA=mRNA /DB_XREF=gi:10437640 /UG=Hs. 306778 Homo sepiens cDNA: FU21524 fis, ch AKQ25177	d AK025177	1.51
	solute cerner family 12 (potasisim/chloride transporters), member 4	AF054506	1.51
	procelagen-bysine, 2-aragidutante 5-dianygenase (pysine hydraxylase) 2	N754404	1.51
	deroncooms 21 open reading frame 108	NH_014825	1.51
	thyroid transcription factor 1	6006221	1.51
	forthwal but it	NM_012188	1.51
	mbit cadde symthase (neuronal)	U31466	1.51
	under roundation t	NM_019055	1.51
	programmed death ligand 2	NM_025239	1.51
	NOWAND PROBLEM BUILDING PROBL	206410_MA	5.
	oranic process	NH 004256	5 5
	Pypothetical protein	NM 016387	5 5
	carbohydrate (N-acehyducosamine 6-0) sutitotransferase 4	NM 005769	5
	coagulation factor VII (serum prothrombin conversion accelerator)	NH_000131	15.1
	protocacherin 17	NH_014459	1.51
	refinal pigment spithefium-derived rhodopsin homolog	NM_006583	1.51
	Conservato includes gib/1931 1/0EF = Home supiens clone 23608 mRNA sequence. /FEA=mRNA /DB_XREF=gi:2795913 /UG=Hs. 6220 Home supiens clone 23608 mRNA sequence	AF038193	1.51
	reported protein 11319	NM_024614	1.51
	Acongration latter in the property of the latter in the contraction from a ration from a	\$E965369	:S:
	Control to the regard of the second of the s	MA_001213	<u>.</u>
	nows the interrogations are excepted, two contains, stort cytopastint (all, 3) [BAR13] in the contains are contained to the c	KM_012313	<u>.</u>
	stratification in	ABU023/3	5.3
	hypothetical protein [U1394]	NM 024848	<u>.</u>
	tachydain receptor 2	NH 001057	<u>.</u>
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myssa, nawy porjectore 11, smooth muscle	AW771910	5 5
income receipt compared to the contract of the	106641	1.51
profit arrays designed from the profit of th	NH_012387	1.5
synodal acrom. L'habbari	282471	1.51
6 untigen 4	NH_001474	2
Concersus includes gb.ALOSQ328 /OEF=Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelinoligodendrocyte glycopratein MGG, (par ALDSQ338	s. (par AL050328	5
practicating growth factor, beta neceptor III (belady)can, 300kb)	KM_003243	5 5
(UM4 ambgan leutocyte ambgan)	7101010	
Comment information (AFLETS) AND SEFER AND SEF	24 (h AW771015	5
Consensus includes do 8.000975, DE Flore HARE 344306, mRN, parial cts. FELTERRIN (PROD=libroom terretor for INAGE 344316) DB XRE = or 1.2803026 A 8.000975	26 A BC000975	1.51
Companies includes gb.A.(031686 (DEE = Human DNA sequence from clone 98112.3 on chromosome 20q12.1-13.2. Contains a Nouspel type zinc-finger protein pseudogene, a 2MF127 pseur AL031686	pseur AL031686	1.51
Consumus includes giv.86.478428 /F.EA=EST /DB_XREF = gi:13410807 /DB_XREF = eai:602523839F1 /KLONE=1MAGE:4642353 /UG=H;.326416 Homo sapiens mRIV;. CDVA DIGZ-p564H1911 816478428	H191f BG478428	1.5
P311 protein	U36189	<u>-</u>
hypothetical protein MGC4643	AAB24369	<u>5</u>
producturation (in receptor 3 (subtype EP 3)	038299	<u>.</u>
interferon-induced, hepatitis C-associated microtubular aggregate protein (44kD)	NM_006417	5
UNAVESS gene product	241145 24 4446466	2
CONTROL DE SECUENCE DE LA SECUENCIA DE LA SECU	104 08 74440400	<u> </u>
NAMES TO STORY OF THE STORY OF	M15465	<u>.</u>
pytywane man en	NN 021930	5
endocheilia PAS domain protein I	AF052094	1.51
TAFE-Bite RNA polymerae II, p300/187-ussociated factor (PCAF)-ussociated factor, 65 kD	A1005317	1.5
fibrinosen. A sizha portrespide	NM_000508	1.51
GCL2-related consists titler	NM_014204	1.51
hypothetical protein	NM_012066	1.51
Onal (Hsp40) homolog, subtamily B, member 5	AX023253	1.5
cytodrome P450, subtanily 1 (dozin-inducible), potypeptide 1 (glaucoma 3. primary infantile)	AU154504	<u>.</u>
solute certier family 28 (sodium-coupled nucleoside transporter), member 1	062966	<u>.</u>
ects related provien (2) complets, subunit 4 (20 Li)	A-019868	2 2
person (or systems) processing states, the first in paramogen activator innition type 1; memoer 1	NW 001249	5 5
Presente month of containing 10	AF220122	-5.
gb:8C001957.1 /DEF = Home supiens, Similar to KIAA0144 gene product, clone MGL:761, mRVA, complete cds. /FEA=mRNA / PR00=Similar to KIAA0144 gene product / DB_XREF = gi:128050 8C001957	:8050 BC001957	1.5.
hypothetical protein	BF055311	1.51
Kruppel-kite factor 2 (lung)	NM_016270	1.5
The state of the s	NM_003174	<u>.</u>
Moderated order receptor (NM_005060	5
acrossiscent is receipted.	44679297	5 5
hypothesia protein FLIZS1	NM_025087	5
hypothetical protein SAAP31	A8059408	1.51
Consuments includes gb-W 003738.1 / DEF=Home sepiens chromosome 21q2.1.1 anonymous mRNA sequence. FEA=mRNA /DB_XREF=gi:2197087 /UG=Hs. 266526 Homo sepiens chromoso A 6003738	тоѕо- АF003738	1.51
hast shock 70kD protein the 1	085730	5
Popular Inter-activities protein 2 (p43)	NM_024534	<u> </u>
orphic contacts	U07820	5
Fe tragment of left. high affinity I, receptor for, gamma polypoptide	NH_004106	1.51
Roufen 1	NM_006487	1.51
frequent homolog (Drzocytia)	NM_014286	<u>.</u>
Typicanies-evillad protein	NA_000550	<u> </u>
introduced in the control of the con	NM 014763	5
KDAO020 protein	AL136712	2.
potazajum voltage-gated Channel, KQT-like subtamity, member 1	AF051426	
to the state of th	A/829081	<u>.</u>
Improved the Part of the Control of	NM_023016	<u>.</u>
small inducible extrings the A (Co. (co.) promoted in the control of the control	A800021	5 5
hypothetical protein FU20513	NN_017855	1.51
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almy (memberse) ammoseroticus (minoceroticus N. ammoseroticus M. microsomal ammoseroticus (013, p150)		1.51
A brane (PEA) anchor crotain 1		<u>.s</u>
potassium voltage-gated channel, Snai-netred subfamily, member 3		1.51
nuclear receptor co-repressor 2		<u>.5</u>
Consumble includes gb:86289001 FEA=EST / DB_XREF = gi:13044404 / DB_XREF = gi:502381262F1 / CLONE=IHAGE:4499078 / JUG=Hs:101282 Homo sepiens cDNA: FLD21238 fs, clone CO 86289001		<u>.</u> 5
DEFE 4 protein		<u>.</u>
bumor necrosis factor receptor superfamily, member 11b (coteoprotegerin)		<u> </u>
Consumus includes gb:8531136 /FEA=EST // DB_XREF = g:9759781 // DB_XREF = est:601278315F / KIONE=INAGE:3610539 // UG=H: 8982 ESTs, Highly similar to KIAN 1305 protein H: Apple 8533 1136		<u>.</u>
Conservate includes gd:565761.1 / DEF anti-colorectal carcinoma heavy chain=gtycoprotein (AVA6-50 specific IgG1 kappa human, 19:9 hybridoma, antibody 11(BNS19:9, mRNA, 1915 nt., v. 265/61.		5
frizzled homolog 7 (Drasophila)		5 3
hypothetical protein similar to small 6 proteins, especially RAP-2A	2	<u>.</u>
NUDPH cookers 1		5
serine protease inhibitor, Kazal type, S	9	<u>.</u>
fibronactin leucine rich transmembrane protein 2		-5.
(61-142)	AW207448	1.51
small nuclear ribonucleoprotein 70t0 potypeptide (RNP antigen)		<u>.5</u>
6 protein-coupled receptor binase 7	NM_017572	1.51
Pryodhetical protein FU23059	AK026712	2
gb.AF098641.1 / DEF = Homo sapiens (D44 isoform RC (CD44) mRNA, complete cds. / FEA=mRNA / GEN=CD44 / PROD=CD44 isoform RC / DB_XREF = gi:3832517 / JUG=Hs.396278 Homo sapie.	AF098641	15.
RAA1117 protein	AL162056	<u>.</u> 5
hepatocyte nuclear factor 3, beta	AB028021	<u>.</u>
banca necrosis factor, alpha-induced protein 2	NH_006291	2.
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e deientegrin and metalloproteinase domain 12 (mettrin alpha)		S, i
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amyloid beta (A4) procursor protein (protesse nezin-il, Adheimer disesse)		S,
odd-stipped-related 2A protein	A/811298 1.	8
Putable prostate cancer tumor suppressor	A884858 1.	S,
protein tyrosine phosphatase, receptor type, M	NM_002845 1.1	8

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	hypodhetical protein FU12765	852	.50
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	hypothetical protein PRO1777	8	8
	protein tyrosine phosphatase, receptor type, F		8.
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	s, subfamily A member 3 (hematopoietic cell-specific)		8
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	Consumus includes gb.XX027151.1 (DEE=Homo supiers CDNX FU23498 fis, close UNG02683. FEA=mRNA /08, XREF=gi:10440206 /UG=Hs, 306904 Homo supiers CDNX FU23498 fis, cl XX027155		8
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	Consumus includes gb.A1350339 FEA=EST 708_XREF=gi-4087545 /708_XREF=gi-40835406.11 KIONE=INAGE:1910362 /106=Hs.144563 tryptophan hydroxytase (tryptophan S-monocony, A1350339		S
	DVZ7256671018 protein		s
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Corsensus includes gb-W024553.1 / DEF = Homo supiers cDN4: FUZ0900 fis, clone ADIX403593. FEA=mRNA / DB_XREF=gi: 10436861 / UG=Hs. 306687 Homo supiers cDN4: FUZ0900 fis, clone ADIX4034553	· AX024553	<u>2.</u>
SP110 nuclear body protein	NM_004510	9.
dess-I MK-restricted T cell associated molecule	NN_019604	<u>.</u>
dane FLB1727	NM_016414	3.
protein A	NM_019858	3.
Consensus includes g-3/207792 /FEA=EST //DB_KREF=gi:3769734 //DB_E=HST-08903.x1 //CLONE=IMAGE:1953029 //JE=HS.306019 ESTs. Wealby similar to ALU7_HUMAN ALU SUBFF A/207792	7 AI207792	3.
similar to 568401 (cattle) glucose induced gene	NM_012261	3.
hypothetical protein McCs457	8600038	95
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A CONTRACT OF THE CONTRACT OF	MM_031277	8
soute Carber Tamiy 23 (mitochondria carber, Graves disease autoantigen), member 16	A1827990	3.
secretary cerner membrane protein 1	AL049223	8.
Merecheldase (protoporphyria)	NM_000140	<u>.</u>
haptoglobin-valated protein	NM_020995	3.
Consensus includes go.XXX24455.1 / DEF = Home suplens mRNA for FU00047 protein, purtial cds. /FEA=mRNA /EEN=FU00047 /PR0D=FU00047 protein //08 XRFF=qi:10440423 /M6=Hs.		8
caldum channel, voltage-dependent, alpha 2/delta subunit 2	NM 006030	95
Consensus includes ab-XXX26682.1 / IDEF = Homo stations cDNV: FLL23029 fs. close UKG01883. FEA=#RNA / IDB XRFF = i:10439589 / IIG=Hs 106864 homo saniens cDNA: FLL23029 fs. close UKG01863	AX026682	5
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ofment, of oblicating, intermediate polypepode 2	AF250307	<u>s</u>
simpler to myosin neavy chain, cardiac muscle alpha isoform (myht-alpha) (m. musculus)	AK000947	3.
phosphomostide-3-tonese, regulatory subunit, potypeptide 2 (p85 bets)	NM_005027	3.
CONSUME SOLVA 78300 PEAEES FOR ARE = 9:4371526 FOR AREF = estima 39-01.x1 ALONE = IMAGE.2160504 FUG = H. 192789 ESTS, Weakly similar to ALUG - HUMAN ALU SUBFF A478300	: N478300	8.
Cholmergy receptor, necebrar, alpha polypopide 6	NM_004198	.
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The List process under related to the myoronic dystropoly protein kindse	NM_003607	8.
ILLANDAR media	NA_004865	9.5
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hypothetical protein MG(2376	NM D23930	9
singiturationae 8 (alpha-N-acetylneuraminate: alpha-2,8-sialytransterase, GD3 synthase) A	132867	9
T-best 4	NM 018488	S
enaplastic tymphoma timase (Ki-1)	BF057492	9
cytoplasmic FMRP interacting protein 1	80005097	8
metanome antigen, tarrity A, 3	8000340	8
Phesis blood group-associated glycoprotein	AF031549	8.
eythrapoietin	AF053356	3
ubiquitin specific protease 9. Y chromosome (Drosophils fat facets related)	NM_004654	35.
phospholipid scramblase 1	NM_021105	1.49
brackfishin receptor B1	NH_000710	1.49
homolog of yeast ATP 1.2	AF070584	67.
NAVIM dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19k0, ASHI)	A723057	69.1
Imphocyte artigen 95 (activating NK-receptor, NK-p44)	NH_004828	67:1
popolykupinove deriminase type i	NM_013358	1.49
A Montes (PRIA) archic protein (polite) 9	NM_005751	1,49

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COTSMITHS INCLOSES \$1 / DEF = Human DNA sequence from clone RP3-47SN 16 on chromosome 6912.3-21.2. Contains the genes for CIG4A, pre-T cell receptor alpha, a novel protein AL035SB7	
BC004153 Bridging profein 4	
M. Spirit	
photophalogisarine receptor	
Consensus includes 90-X234255.1 (DEF = Homo sapiens clone KM36 immunoplobulin light chain variable region mRNA, partial cis. (FEA=mRNA, PROD=immunoplobulin light chain variable xezistas	
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similar to DNA-directed RNA polymertes (133 t.D.)	NH 019014	9
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Phy-1 cell surface antigen	AA218868	. 49
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popers protein 3	NM_022361	.
Outsty Mich (1734/St.m32.80); 11 Home supriens (DNA, 3; end /clone=IMAGE.2391924 /clone_end=3 /gp=A/738452 /gj=5100433 /ug=Hs, 203286 /ten=533	A1738452	6 :
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hypothetical protein FU10381	NM_018080	1.49
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DA-binding protein IDA (militition of the DA and Azin complex)	NH 025212	9
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cyclic nucleotide gated channel beta 1	U58837	1.49
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ATPase, Class VI, type 11A	AL161996	1.49
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tasue inhibitor of metalloproteniase 1 (enythroid potentiating activity, colladenase inhibitor)	NH 003254	9
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retinais acid receptor-beta associated open reading frame	NM_015854	.
homeo bos 01	NM_024501	1.49
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hypothetical protein FU10998	NH_018294	. 69
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19 fs., clore (CNOSO77. FEA=mRNA /OB_XREF=g;1021088 /VG=H; 32158) Homo supiens cDNA FUZ0779 fs., clore (CNOSO77. FEA=mRNA /OB_XREF=g;1021081 /VG=H; 306504 Homo supiens cDNA FUZ0779 fs., clore WENB100255 (MCZp) fill continues bVCZp/SE1123121; FEA=mRNA /OB_XREF=g;7669981 /VG=H; 306504 Homo supiens continues		
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achesto-acute complex-like 1 (Drosophila)	AW950513
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serine/thruconine binase 38	AF034187
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CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	8F693956
solute carrier family 2 (facilitated glucose transporter), member 3	AL110298
interleubin I receptor antagonist	BE563442
AAD23 homolog B (S. cerevisiae)	19362
allografi inflammatory factor t	AF299327
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engrafied homolog 1	NH_001426
serine/Directime kinase 3 (STE20 homolog, yeast)	NM_006281
FAT tumor suppressor homidog 2 (Orasophits)	NH_001447
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übber celi lectin-like receptor subhamily F, member 1	NM_016523
colote carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	NM_022829
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sine acudis hamaaba hamalag 1 (Drasaphisa)	Z86500_MM
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hypothetical protein FU13576	NM_022484
tour and a half LIM domains 2	NN 001450
met proto-ancagene (hepatocyte growth factor receptor)	86170541
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OP-ribosylation factor-like 7	AW450363
moothetical cretein FU12983	NM 024856
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woodbelcal profein FU 1236	NM 024902
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Just (Hsp40) homolog, subfamily 8, member 5	NW 012266
therefore intracellular channel?	AC303C14

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hypothetical protein FU13511	NM 004575	1 2
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a processor described in the contract of the c	NM_004694	1.37
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	hypothetical protein FU13055	AA209463	1.36
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	carbohydrate (H-exetylducosamine 6-0) sufformer terase 7	AL022165	1.36
	alpha-antitylacyl-Cod racemase	AF047020	9
	protein linnes C, mu	NM_002/42	9 5
	anisodendinate, dette, synthase 2 (sidenoblastic/hypochromic anemia)	178587	9.
	6 protein-coupled receptor (SL2	NM_018485	9 5
	hypothetical protein FUZ3510	02/\$20 WN	95.
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	Comments include gove 3351-11 (LVC include a pages) and a page comment of the com	U7 H AWS03390	1.36
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	intertwitin 1 receptor, type II	NM_004633	1.36
	chromodownia halicase DNA binding protein 2	NM_001271	1.36
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	gamma-aminobutynk add (GABA) A receptor, gamma 2	NM_000816	<u> </u>
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byptone dafta 1 · ·	NM_012217	1.36
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equatement growth factor receptor (enythrochestic levidemia viral (v-erb-b) oncogene homolog, avian)	NM_045053	7.5
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(Do GT) has activating protein 8	A533284	1.33
hypothetical protein FU20071	NM_017653	1.33
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hypothetical protein FU13110	NM_022912	F :
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hypothetical protein FU11539	NM_024748	<u>e</u> :
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sealer carrier family 4, micro activators, member 3,	NH_005070	. E.
Money (neutrol immediate early gene, 3	A1871287	9

dystrogicus 1 (dystropins-essociated gykcoprotein 1)	AW411370	1.33
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(GL43 protein	NM_016027	1.33
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potantium voltage-gated channel, KQT-libs subtamity, member 2	D82346	1.33
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hypothetical protein MG(3048	NM_024052	3
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zint finger protein 278	AF254087	1.33
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cyclin-dependent binase 5, regulatory subunit 2 (p39)	R51311	1,33
UDP Extraolocitik beta 1, 4. galaxton/franse, polypeptide (U10473	13
cholinarys receptus, nicobinis, alpha polypeptide 5	NM_000745	60
regulatur of Exercisis signalling 6	AF073921	1.33
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protein kinase, lysine deficient 1	A1768512	1.32
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estrogen receptor 1	NM_000125	<u>.</u>
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sodium channel, writings-gartel, type II, beta polypepide	AF107028	<u> </u>
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UMU13 is gane product	NM_014635	<u>.</u>
hypothetical protein FLR1522	NM_024526	5
CD4 antigen (sudocyte antigen)	196627	<u>-</u>
sialytransfarace 4(forta-galactrosidase alpha-2, 3-sialytransferase)	KM_006278	<u>-</u>
zinc finger protein 41	A1927984	<u>-</u>
nuclear receptor co-repressor 2	283390	5
matrix metalloproteinuse 26	NM_021801	<u>.</u>
phosphodestress 9A	NM_002606	<u>-</u>
cardinomity one, ambigue-related cell adhesion molecule 1 (billary glycoprotein)	M69176	<u>-</u>
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hypothetical protein FU23053	NM_022907	1.30
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dops decembosylable (aromatic Lisatrino ecid decarbosylable)	NM_000790	1.30
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solute carrier family 7 (cationic arrino and transporter, y+ system), member 2	NM 003046	200
hypothetical protein FLIZ0051	NM_019087	1.30
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